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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 3, 2006, 00:41:37 ; Search time 941 Seconds
(without alignments)

2899.994 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVEKNTRKIAMVGSGMI.....GSIDEVKEMQKAIAALDASK 330

Scoring table: BLOSSUM62

Xgapext 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 979352 seqs, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB Seq length: 0

Maximum DB Seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/abs/ABSWEB_spool/US09390846/runat_02032006_104243_5094/app_query.fasta_1
-DB=Published_Applications_NA_Main -QWMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0 -HOSTCPU=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blossum62 -TRANS=human40_cdi -LIST=45 -DOCAIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTfmt=pct -NORM=ext
-HSIZE=501 -MINLEN=0 -MAXLEN=501 -WAIT=100 -LONGLOG -DEV TIMEOUT=120
-NO_NMAP NEG SCORES=0 -DBPBLOCK=100
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6 -FGAPEXT=7

Database : Published Applications_NA_Main:*

1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	1034.5	61.3	1785	3 US-09-216-393-311 Sequence 311, APP
2	1034.5	61.3	1785	3 US-09-216-393-311 Sequence 313, APP
3	1034.5	61.3	1785	6 US-09-216-393-311 Sequence 311, APP
4	1034.5	61.3	1785	6 US-09-216-393-311 Sequence 313, APP
5	880.5	52.2	960	6 US-10-369-493-41525 Sequence 41525, APP
6	873.5	51.7	957	6 US-10-369-493-35128 Sequence 35128, APP
7	873.5	51.7	960	6 US-10-369-493-38176 Sequence 38176, APP

Sequence 38561, A
Sequence 44435, A
Sequence 35747, A
Sequence 40766, A
Sequence 31700, A
Sequence 34210, A
Sequence 46924, A
Sequence 41082, A
Sequence 40205, A
Sequence 42814, A
Sequence 37272, A
Sequence 34088, A
Sequence 41907, A
Sequence 3855, APP
Sequence 34859, A
Sequence 43537, A
Sequence 32732, A
Sequence 34088, A
Sequence 41907, A
Sequence 34859, A
Sequence 43537, A
Sequence 26509, A
Sequence 34351, A
Sequence 34654, A
Sequence 42545, A
Sequence 56, APP
Sequence 23825, A
Sequence 23812, A
Sequence 46543, A
Sequence 38013, A
Sequence 4543, A
Sequence 40390, A
Sequence 42017, A
Sequence 4058, APP
Sequence 46760, A
Sequence 40390, A
Sequence 311, Application US/09216393

RESULT 1
US-09-216-393-311
; Sequence 311, Application US/09216393

; Patent No. US200101447A1
; GENERAL INFORMATION:
; APPLICANT: Milthausen, Michael James
; TITLE OF INVENTION: TOXOPASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
; USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US-09-216-393
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08-1994, 825
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 311
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Toxoplasma gondii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (75)
; US-09-216-393-311

Alignment Scores:
Pred. No.: 4.91e-111
Score: 1034.50
Percent Similarity: 77.3t
Best Local Similarity: 60.1t
Query Match: 61.3t
DB: 3

US-09-390-846-2 (1-330) x US-09-216-393-311 (1-1785)

Sequence 313, Application US/09216393
Patent No. US20010014447A1

Sequence 313, Application US/09216393	Patent No. US200101447A1
GENERAL INFORMATION:	
APPLICANT: Milhauser, Michael James	TITLE OF INVENTION: TOXOPASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND TITLE OF INVENTION: USERS THEREOF
FILED REFERENCE: TX-1-C2	CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18	EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19	NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin Ver. 2.0	SEQ ID NO: 313
LENGTH: 1785	TYPE: DNA
ORGANISM: Toxoplasma gondii	JS-09-216-393-313
Alignment Score:	
Aligned, No.:	4,916-111
Score:	1034.50
Percent Similarity:	77.3%
Best Local Similarity:	60.1%
Query Match:	61.3%
DB:	3
Gaps:	1
US-09-390-846-2 (1-330) x US-09-216-393-313 (1-1785)	
Dy	9 Arg Pro Dsle Ala Val Val Gly Arg Gly Met Leu Glu Gly Met Ala Phe Ieu Cys B
Dy	109 AGAAAGGGGCGCTGTGATGGCTGGATGATGTTGGCAGCTATGGCTACTTGTGTC 168
Dy	29 Ser Leu Arg Glu Leu Gly Asp Val Val Leu Phe Asp Val Val Pro Asn Met Pro Met Gly
Dy	169 GCTCTCGTGAGCTCTGCAGTCCTCTACGTTGTTCAAGGTATGCCGGAGGGT 228
Dy	49 Lys Ala Met Ap Ile Ser His Asn Ser Ser Val Val Asp Thr Gly Ile Thr Val Tyr Gly
Dy	229 AAGGCCATCTGAGCTGGCCATGTGACCTCGTGACCTCGTGACCAAGGTTGGCTGAC 288
Dy	69 Ser Asn Ser Ile Glu --- Cys Leu Iys Gyl Ala Asp Val Val Ile Ile Ala Gly Ile 87
Dy	289 GAGTACTCTAACGAGCCGCTCACGGTGAGCTGGACTGGAGACGATCTGGCTCCCTCTAAC 348
Dy	88 Thr Lys Ile Pro Gly Lys Ser Asp Iys Glu Trp Ser Arg Met Asp Leu Ile Pro Val Asn 107
Dy	349 ACCAAGGTGCCGGCAAGGCCGACTCGGAACGACTGGACATGGACGATCTGGCTCCCTCTAAC 408
Dy	108 Ile Lys Ile Met Arg Glu Val Gly Ala Ile Ile Lys Ser Ile Cys Pro Asn Ala Phe Val 127
Dy	409 TCGAAGATCATTCATGCCAGATCGTCAAGAACATCAGAAAGTACTGCCCAAAGACCTTCATC 468
Dy	128 Ile Asn Ile Thr Asn Pro Leu Asp Iys Val Met Val Ala Ala Leu Glu Glu Ser Ser Ile Leu 147
Dy	469 ATCGTGTGTCACCAACCGCTGACITGCAAGTGTGGAGGGCTCTGGCT 528
Dy	148 Pro His Ile Arg Glu Cys Gly Met Ala Gly Met Leu Asp Ser Ser Arg Phe Arg Arg Met 167
Dy	529 CGGACCCACATGATCATCGGTATGGCTGTGATGCTCGATCTGGCTGTCCTGGCTAC 588
Dy	168 Ile Ala Asp Lys Ile Glu Val Ser Pro Arg Asp Val Glu Gly Met Val Ile Gly Val His 187
Dy	589 GTCGCCAGCGCTGTCATGCCGCTACATTACGTGAACTACCCGACTACCCGATCCAGAAC 648
Dy	188 Gly Asp His Met Val Pro Leu Ser Arg Tyr Zala Thr Val Ile Gly Ile Pro Leu Ser Glu 207
Dy	649 GGGGACTGCACTGGTCCGGCTGTGTCATGCCGCTACATTACGTGAACTACCCGACTACCCGATCCAGAAC 708
Dy	208 Phe Val Lys Lys Gly Trp Ile Leu Glu Lys Val Asp Ile Val Gln Lys Thr Lys 227
Dy	709 TCTACAGGAAGGGCTGAGTAGTCACTGGAGAAGGAGCTGGAGGATGCTGAGCACCAA 768

; TYPE: DNA
; ORGANISM: Toxoplasma gondii
; US-10-321-856-313

Alignment Scores:
Pred. No.: 4.91e-111
Score: 1034.50
Percent Similarity: 77.3%
Best Local Similarity: 60.1%
Query Match: 61.3%
DB: US-09-390-846-2 (1-330) x US-10-321-856-313 (1-1785)

Qy 9 ArgProlysileAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
Db 109 AGAAAGAAGTGGCCATGATGTTGGCTTGATGATGGTCACATGGGCATACCTGTGC 168

Qy 29 SerLeuArgGluLeuGlyAspValValProLeuAsnMetProMetGly 48
Db 169 GCTTCGGTGGCTCGCTAACGATGTTGTCAAACGTTACGATGTTGCAAC 228

Qy 49 LysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrValtryGly 68
Db 229 AAGGCTTGTGACTGACCCTGACCCATTGACCTTGCAACCAACGTTCCGTCGTGCT 288

Qy 69 SerAsnSerTryGlu---CysteulyssGlyAlaAspValValIleIleThrAlaGlyIle 87
Db 349 ACCAAGGTGCCGGCAAGCCGAATCGAGTCGGACTGCGTTAACGCCGGCTG 348

Qy 88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspIleLeuProValAsn 107
Db 289 GAGTACTCTTAAGGGCGCTCACCGTGGACTGCGTTAACGCCGGCTG 348

Qy 108 IleLysIleMetArgGluLeuGlyAlaAlaAlaLysSerIleCysProAsnAlaPheVal 127
Db 409 TCGAAGATCATGTCGGGATCGTCAAGAGATAGCCCAAAGACCTTCATC 468

Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerGlyLeu 147
Db 469 ATCGTGTCAACCAACCCGCTCATGGTCAAAGTCATGGTCAGGGCCCTTCGGTC 528

Qy 148 ProHisIleArgIleCysGlyMetAlaIleGlyMetLeuAspSerSerArgPheArgMet 167
Db 529 CGGACCAACATGATTCGGGATGGCTGCTGCACTCTGTCGACTCTGGCTTCGGCGATAAC 588

Qy 168 IleAlaAspLysIleGluValSerProArgAspValIleGlyMetValIleGlyValHis 187
Db 589 GRGCCACGCGCTGTCGTCGTCACCGTCATCGCACAC 648

Qy 188 GlyAspHisMetValProLeuSerArgTyraIleProLeuSerGlu 207
Db 649 GGCGACTGCACTGTCATGCCCTCCGGCAACGACTACCCGATCCAGAG 708

Qy 208 PheValIleSlyIlePheIleGlyGluValAspAspIleValGlyIleIleThrLys 227
Db 709 TTCAATCAGGACGGCTGAGTCAGGAGAGCTGAGGAGATCGTGAAC 768

Qy 228 ValAlaGlyGlyGluIleValArgLeuIleGlyGlnGlySerAlaTyrralaProGly 247
Db 769 GTCCTCGGGCAAGATGCCCTTCGGCTGAGTCAGGAGCTGAGGAGATCGTGAAC 828

Qy 248 AlaSerAlaIleGlnMetAlaGluSerIleTyrralaLeuGlyIleGlySerAlaMetValCys 267
Db 829 GCTATCCGGTGTGCCATGGCAAGATGCCCTTCGGCTGAGTCAGGAGCTGAGGAG 888

Qy 268 SerCystyLeuGlyGlnIleGlyGlyValGlnAsnIleSlyIleGlyValProCysVal 287
Db 889 AGGTGTAATGCAACGAGTGAAGACATGTTCAATGCTGGCTGAGGAGCTC 948

Qy 288 IleGlyGlyArgGlyValGlyIleValGlyIleLeuGlnIleLeuGlnGluArgGln 307
Db 949 ATGGAGACGCCGATGGAGCCGTCAGCTGAGCCGTCAGCTGAGGAGAGAG 1008

Qy 308 GluLeuGlnGlySerIleAspGluValValAspGlyMetGlnIleAlaAlaLeuAsp 327
Db 1009 CAGTTCAGAACTCCGTCGACGAGTCATGGCGCTCACAAAGCGGTCAAC 1068

RESULT 5
US-10-369-493-41525
Sequence 41525, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-101520521 B
CURRENT APPLICATION NUMBER: US 10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SEQ ID NO: 41525
LENGTH: 960
ORGANISM: SPHINCOMONAS
US-10-369-493-41525

Alignment Scores:
Pred. No.: 2.88e-93
Score: 880.50
Percent Similarity: 70.7%
Best Local Similarity: 53.9%
Query Match: 52.2%
DB: 6
Length: 960
Matches: 173
Conservative: 54
Mismatches: 89
Indels: 5
Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-41525 (1-960)

Qy 9 ArgProlysileAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
Db 7 CGCAAGAGGATCGGCGATCGCTCCGGCATGATCGGGCGACCCCTCCGGCACCTCGCT 66

Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
Db 67 GCATCAGGAACCTGGGATATGTCCTGTTGACATTCGCGGACATTCGGCAGGGC 126

Qy 29 SerLeuAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleIleThrValtryGly 68
Db 127 AACGGCGCTGACATGCAAGTCGGACAGTCGGACCTGGCTGATGCCAACCTCAAGGGC 186

Qy 69 SerAsnSertryGluCysLeuIleGlyAlaAlaAlaLysSerIlePheValIleLeuGlyIleIleThrLys 88
Db 187 GCGAACGTTACGAGGACATTCGGGATTCGGGCGGACCTCTGGATCCGGATTCGG 246

Qy 49 LysAlaAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleIleThrValtryGly 68
Db 127 AACGGCGCTGACATGCAAGTCGGACAGTCGGACCTGGCTGATGCCAACCTCAAGGGC 186

Qy 89 LysIleProGlyIleSerAspIleSerGluItrpSerSerArgMetAspIleLeuProValAsnIle 108
Db 247 CGCAAGGCCGGC-----ATGAGCCGCGAGATCTCTCAAGACCAACCTGATC 291

Qy 109 LysIleMetArgGluValGlyAlaAlaAlaLysSerIlePheValIleLeuGlyIleIleThrLys 128
Db 292 GGCGTGTGATTAAGGCCGCTGCCGCGAGCTGCCGAGCGGCCATGCCGAGCG 351

Qy 129 AsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluUserSerGlyLeuPro 148
Db 352 TGATCACAACCGCTCAACGCTCATGGCTGGGCGCTCGGCTCGGCCTGCG 411

Qy 149 HisIleArgGlyGlySerGlyMetIleGlyMetIleAspSerSerArgPheArgArgMetIle 168
Db -----

Qy 129 AsnIleThrAsnProLeuAspValMetValAspSerGlyLeuPro 148
 Db 352 TGCATCACAACCCGGCTGACGCCATGGTCGGCGTCAAGAAGTCGGCTCGCG 411
 Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgArgMetIle 168
 Db 412 AAGAACAGGTCGTCGCAcCATGGCTTCGACGCTCGCTGTTCTT 471
 Qy 169 AlaAspLeuGluValSerProArgAspValGlyMetValGlyValHisGly 188
 Db 472 GCGGAAGAAATTCAACGGTTTCGTCAGGACTCACCGCCTTCGGGGTCATGGC 531
 Qy 189 AspHisMetValProLeuSerArgTrpValAlanylSerGluPhe 208
 Db 532 GACACCATTGGTCCCCTGGCTGGCGTATTCCACGTGGCGGGTACCGATCTC 591
 Qy 209 ValLysLysGlyTrpIleLysGluGluValAspPheLeuValThrIleVal 228
 Db 592 GTCAAATGGATGGCTGGTGAACCCCCGAGTCITMAGGAGATCATCCAGGCACCCGTGAC 651
 Qy 229 AlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrAlaProGlyAla 248
 Db 652 GGGGGCCGGAAATCGTGGCTCTTGAAAGACGGCTTATTAGCCGGCCGCT 711
 Qy 249 SerAlaIleGlnMetAlaGluSerIleLeuGlyLeuGlySerArgValMetValCysSer 268
 Db 712 TCGGCTATCGAAATGGCGGAATCTACCTCAAGAACAGAGCGCTTCCTCCCGCTGT 771
 Qy 269 CystTyreLeuGlnGlyGlnTyrglyValGlnAsnHistYleLeuGlyAlaProCysValIle 288
 Db 772 GCCCACCTTCGGCCAGTATGGCTGAGACGACATGTATGTCGGCTGCCAACCATCATC 831
 Qy 289 GlyGlyArgGlyValGluIleLeuGlySerIleLeuGluLeuGluLeuGluArgGlnGlu 308
 Db 832 GGTGGCGGGTATCGAGGGCTCATCGAGATCGAGCTGAAGAAAGGCCGCC 891
 Qy 309 LeuGlnGlySerIleAspGluValAspGluMetGlnyAla 322
 Db 892 TTCCAGAAATCGTCGGCTGTCGTCGTCGTTGGAAAGCC 933

RESULT 9
 US-10-369-493-44435
 ; Sequence 4445, Application US/10369493
 ; Publication No. US200302333675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-1010(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-01
 ; SEQ ID NO: 4435
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Rhodopseudomonas palustris
 US-10-369-493-44435

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
 Db 7 CGCGATAAAATGCTTGTATGGCTCGGGCAAGATGGCGTACCGTGGCACTATGGTC 66
 Qy 29 SerLeuIargGluLeuGlyAspIleValLeuIpheAspValValProAlaMetPheMetGly 48
 Db 67 GGTCGAAGAGCTGGCGACGGTGGCTGTTGCAATTGGCAGGGTGGCGAGGGC 126
 Qy 49 LysAlaMetAspIleSerHisAsnSerSerValAspThrGlyIleLeuValIrgly 68
 Db 127 AAGGCCCTGAGATCGGGAGTCCTGGCGTCGAGCTCAAGCTGACGGTTTCGATCTCAAGCTGGT 186
 Qy 69 SerAsnSerIleGluCysIleLeuLysGlyAlaAspPheValIleIleLeuAlaGlyIleLeuThr 88
 Db 187 GCCAATCTCTACGAGCGATCGAAGCCGGCGCTGGTGTATGTCACCGCGGGCTGCGC 246
 Qy 89 LysIleProGlyLysSerAspIlePheGluTrpSerArgMetAspLeuIeProValAsnIle 108
 Db 247 CGCAAGCCGGC-----ATGAGCCGTGACCATCTCATCACATCACCTC 291
 Qy 109 LysIleMetArgGluValGlyAlaAlaIleIleSerIleCysPheAsnAlaPheValIle 128
 Db 292 AAGGATGGAGCACTGGCTGGCTGGTCAAGAGTAACGCCGAGCTGGCTGATCTGATC 351
 Qy 129 AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluUserSerGlyLeuPro 148
 Db 352 TGCACTACCAACCCGCTGAGCGTGGCTGGGCTGAGAAGCCCTGGCTGCG 411
 Qy 149 HisHisArgIleCysGlyMetLeuAspSerSerAspPheArgArgMetIle 168
 Db 412 GCCAAGAAAGGTTGTCGATGGCCATGGCCGGTGGCTCGACTCGCTGCGGTTCCGTTACTTCCTG 471
 Qy 169 AlaAspIleGluValSerProArgAspValGlyMetValIleGlyValIleGly 188
 Db 472 GCGCAGAGTCAAATGGCTGGCTCAAGAGCTGGCTGCGTCGAGCTGGCTG 531
 Qy 189 AspHisMetValProLeuSerArgTrpIleThrValAlaIleProLeuSerGluPhe 208
 Db 532 GATACCATGGTCCGCTGGAAAGTACTCGACCGGCGGAATTCGGCTGCCGACCTG 591
 Qy 209 ValLysLysGlyTrpIleGlyGluValAspAspIleValGlnLysThrIleVal 228
 Db 592 GTCAAGATGGCTGGACCTCGGCGCTGAGTCGAGATCGTGAAGTCGCTG 651
 Qy 229 AlaGlyGlyGluIleValArgLeuIleGlySerAlaProGlyAla 248
 Db 652 GGCGGGCCAGATCTGCTGAGCTGGCTGCGTCGCTGGCTGCTGGCTG 771
 Qy 249 SerAlaIleGlnMetAlaGluSerIleIleLeuGlySerAlaProGlyAla 268
 Db 712 TCGGGATCGCATGGCTGGCGAGCTATCGAAGGCAAGAGGGCTGCGTCGCG 771
 Qy 269 CysTyreLeuGlnGlyGlnTyrglyValGlnAsnHistYleLeuGlyValProCysValIle 288
 Db 772 GCCCACCTCAACGGCAATAGGGCTCAAGACATGTTGCGTGGTGGTGGTGGTC 831
 Qy 289 GlyGlyArgGlyValGluIleLeuGluLeuGluArgGlnGluArgGlnGlu 308
 Db 832 GGCGCAAGGGCTGAGCCATCTCGAGATCGAGCTGGCTGCGTC 891
 Qy 309 LeuGlnGlySerIleAspGluValIleGluMetGlnLysAla 322
 Db 892 TTTCAGACAGGGCTGGCTGCGTCGCGTCAGGGCTGGCTGAGGGC 933

Alignment Scores:
 Pred. No.: 3.67e-91 Length: 933
 Score: 862.50 Matches: 169
 Percent Similarity: 72.6% Conservative: 59
 Best Local Similarity: 53.8% Mismatches: 81
 Query Match: 51.1% Indels: 5
 DB: 6 Gaps: 1

US-10-369-493-35747
 ; Sequence 35747, Application US/10369493
 ; Publication No. US200302333675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.

Qy 249 SerAlaLeuGlnMetAlaGluSerTerLeuLysSerPArgLysTerGlnSerGlnMetValCysSer 268
 Db 712 TCGGCATGGCAATCTTACCTAAAGACAAGAAGCCTGGCTGCCCTGGCT 771

Qy 269 CysteineLeuGlnGlyGlnTerGlyGlnValGlnAsnHisTerLeuGlyValProCysValle 288
 Db 772 GCCACCTTCGGCATGGGTCAAGGACCTTAATGGCTGCCCTGGCTGCCCTGGCT 831

Qy 289 GlyGlyArgGlyValGluLysIleLeuGluTerGluLeuThrAlaGlnGluArgGlnGlu 308
 Db 832 GCGCCGCGGCGTCGAAGCAGATCGAGATCGACCTAACAGAACAGAACAGAAATG 891

Qy 309 LeuGlnGlySerIleAspGluValLysSerGluMetGlnLysAla-----IleLeuAla 325
 Db 892 TTGGAGAGTTGGGGCGACCGTGCAGGGCTGTGACCGAGGCTTGCTCAAATCGGCCG 951

Qy 326 LeuAspAlaSerIle 330
 Db 952 CAGCTGGCTTCGAG 966

RESULT 11
 US-10-369-493-40766 ; Sequence 40766, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; Hinkle, Gregory J.
 ; Slater, Steven C.
 ; Goldstein, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 40766
 ; LENGTH: 963
 ; TYPE: DNA
 ; ORGANISM: Caulobacter crescentus
 US-10-369-493-40766

Alignment Scores:
 Pped. No.: 9.97e-90 Length: 963
 Score: 850.50 Matches: 164
 Percent Similarity: 69.8% Conservative: 60
 Best Local Similarity: 51.1% Mismatches: 92
 Query Match: 50.4% Indexes: 5
 DB: 6 DB: 1 Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-40766 (1-963)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaHeLeuGly 28
 Db 7 CGGGGAAGATGCCCTATGGCCCGGGATGATGGGGACCCGGCCACATGCC 66

Qy 29 SerIleArgGluLeuGlyAspValValLeuPheAspValValProHsMetProMetGly 48
 Db 67 GCTCCGGAAAGCTGGCGAGCTGATCTGTCGATCGCCGAAGCCGG 126

Qy 49 LysAlaMetAspIleSerHisAsnSerValValAspThrGlyTerhrValtyrGly 68
 Db 127 AAGGCCCTTCGACATGCCGAAAGCCTGCGCTGTCGCAAAGGACGGCCCTGGAAAGGGC 186

Qy 69 SerIleSerTerGlyCysLeuLysGlyValAspValValTerAlaGlyTerhr 88
 Db 187 GCCAACTGACTAGCCGACATGCCGAGCTGCTGTCAGCTGTCACGCCGCGTGC 246

Qy 89 LysIleProGlyLysSerAspIleLeuTerGlySerMetAspLeuLeuProValAsnle 108

Db	247	CGCAAGGGGG- -----	-ATGACCCGCCAGCACCTGCTGGGCATCACCTG 291
Qy	109	LysIleMetArgLluValGlyAlaAlaIleLeuSerCysProAsnAlaPheValle	128
Db	292	AAGTCATGAAGGCCGTCGGAAAGGCATCAAAGCTCACGCCCAACGCCCTTCGTCTCATC	351
Qy	129	AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro	148
Db	352	TGCAACCAACCGCTGGAGCCGATGTCGGCCTTGACGAGTCTGGCTTCGGCTCGCCG	411
Qy	149	His His Arg Leu Cys Gly Met Leu Asp Ser Ser Arg Phe Arg Met Ile	168
Db	412	AAGGAAGAGSTCATGCCATGCCGCTTCCTGACTGGCCCGCTTGCTACTTCCTG 471	
Qy	169	Ala Asp Phe Leu Glu Val Ser Pro Arg Asp Val Gln Gly Met Val Ile	188
Db	472	GCTGAAGGCCACGGCGCTTCCTGCTGGAGACATCACGCCCTGGACCTGCGCCGCA	531
Qy	189	Asp His Met Val Pro Leu Ser Arg Tyr Ala Thr Val Asn Gly Ile	208
Db	532	GACGACATGGGCCGAGGGTCTCGTCACTCGACCCTGGCCCTGCCGCGGACTCTG 591	
Qy	209	Val Lys GLY Ile Trp Ile Leu Gln Glu Val Asp Ile Val Gln Lys Thr	228
Db	592	GTCAAGCAAAGGCTGCTGCTGAGCCATGTCAGCAGAACGCTGAGCCATGTCAGC	651
Qy	229	Ala Gly Gly Glu Ile Val Arg Leu Leu Gln Gly Ser Alanine Tyr	248
Db	652	GCGCGCGGAGATCTGCCCTCTCTGAAAGAACCGGGCTGGCCCTTAAGGCCCGAG	711
Qy	249	Ser Ala Ile Gln Met Ala Glu Ser Tyr Leu Lys Baa Darg Lys Arg	268
Db	712	AGCGCATGGCCATGCCGACCTCTGCTGGCCATGCCGTTCCGAGGAAAGGGCTGC	771
Qy	269	Cyste Yle Gln Gly Ctntr Gly Val Gln Asn His Tyr Ile Gln Val Pro	288
Db	772	ACCTACTGTACCGGGCAAGTAGGGCTGAACCACTTAATGTCGGCTGCCGTTGGCTCATC	831
Qy	289	Gly Gly Arg Gly Val Gly Lys Ile Glu Leu Glu Leu Thr Ala Gln Gln	308
Db	832	GGCGCGGGCGCCAGAAAGATCGCAGTGGAAACCAACGACGAAAGGGCATG 891	
Qy	309	Leu Gln Gly Ser Ile Asp Glu Val Val Gln Lys Ala Ile Val Asp Ala	328
Db	892	TTGCCAAGTCGGTCAAGGGCTGAGTCGGTCAAGGGCCATCACAGC 951	
Qy	329	Ser 329	
Db	952	TG 954	
	RESULT	12	
	us-10-369-493-31700		
	Sequence 31700,	Application US/10369493	
	Publication No. US20050233675A1		
	GENERAL INFORMATION:		
	APPLICANT: Cao, Yongwei		
	APPLICANT: Hinkle, Gregory J.		
	APPLICANT: Slater, Steven C.		
	APPLICANT: Goldinan, Barry S.		
	APPLICANT: Chen, Xianfeng		
	TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTIVE		
	PLANTS WITH IMPROVED PROPERTIES		
	FILE REFERENCE: 38-101520521B		
	CURRENT APPLICATION NUMBER: US/10/369,493		
	CURRENT FILING DATE: 2003-02-28		
	PRIOR APPLICATION NUMBER: US 60/360,039		
	PRIOR FILING DATE: 2002-02-21		
	NUMBER OF SEQ ID NOS: 47374		
	SEQ ID NO: 31700		
	LENGTH: 960		
	TYPE: DNA		
	ORGANISM: Rhodobacter sphaeroides		
	US-10-369-493-31700		

Qy 266 ValCysSerCysTyrIleGlnGlyGlnTyrGlyValGlnAsnHistYLeuGlyValPro 285
Db 760 CCAACGATTGCCTACCTGCTGAGTGATGATGATGATGATGAGATATCTATGTTGGAGTCG 819
Qy 286 CysValIleGlyGlyArgGlyValGluLysIleGluLeuGluLeuThrAlaGlnGlu 305
Db 820 ACGATTCTGGGGAGACGGCATTTGAAAGGTATTGAGCTTGAACGATGAGAG 879
Qy 306 ArgGlnGlnIleLeuGlnGlySerIleAspGluValLysGlnMetGlnAsnAlaIle 323
Db 880 AAAGCGACCTTGCTAAGTCCATTGATCTGTTGCAACGTCATGTCGGCACTA 933

Search completed: March 3, 2006, 00:57:35
Job time : 950 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 3, 2006, 00:57:49 ; Search time 405 Seconds
(without alignments)

1786.381 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVEKNTPRKIANVGSMI.....GSIDEVKEMQKAIAALDASK 330

Scoring table: BIOSUM62

Xgapext 10.0 Xgapext 0.5
Ygapext 10.0 Ygapext 0.5
Fgapext 6.0 Fgapext 7.0
Delop 6.0 Delop 7.0

Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Command line parameters:

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-MODEL:frame+pn.model1 -DEV=x1h
-Q=/abs/ABSWEB_spool/US9390846/runat_02032006_104245_5144/app_query.fasta1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX_P2n.rnpbn -MINNATCH=0_1
-LOOPCL0 -LOOPEXT0 -UNITS=b18 -START=1 -END=-1 -MATRIX=biosumG2
-TRANS=human40_cddi -LIST=15 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss03
-USER=US09390846 @CGN 1 1 220 @runat 02032006 104245_5144 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=0 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -KGAPEXT=0.5 -FGAPPOP=6 -FGAPEXT=7
-YGAPPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXIT=7
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Database : Published Applications NA_New *

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2: ./cgns_6/podata/2/pubna/US06_NEW_PUB.seq:*
3: ./cgns_6/podata/2/pubna/US07_NEW_PUB.seq:*
4: ./cgns_6/podata/2/pubna/PCT_NEW_PUB.seq:*
5: ./cgns_6/podata/2/pubna/US05_NEW_PUB.seq:*
6: ./cgns_6/podata/2/pubna/US09_NEW_PUB.seq:*
7: ./cgns_6/podata/2/pubna/US10_NEW_PUB.seq:*
8: ./cgns_6/podata/2/pubna/US10_NEW_PUB.seq:*
9: ./cgns_6/podata/2/pubna/US11_NEW_PUB.seq:*
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11: ./cgns_6/podata/2/pubna/US11_NEW_PUB.seq:*
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13: ./cgns_6/podata/2/pubna/US60_NEW_PUB.seq:*
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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

US-11-156-953-6	;	Sequence 6, Application US/11156953
	;	Publication No. US20060003051A1
	;	GENERAL INFORMATION:
	;	APPLICANT: Cleary, Joseph
	;	APPLICANT: Coleman, Russell
	;	APPLICANT: Harding, Nancy
	;	APPLICANT: Patel, Yamin
	;	FILE OF INVENTION: GENETICALLY PURIFIED GELLAN GUM
	;	CURRENT APPLICATION NUMBER: 012047 0029
	;	CURRENT FILING DATE: 2005-06-20
	;	NUMBER OF SEQ ID NOS: 14
	;	SOFTWARE: FastSEQ for Windows Version 4.0
	;	SEQ ID NO 6
	;	LENGTH: 2862
	;	TYPE: DNA
	;	ORGANISM: Sphingomonas elodea
	;	US-11-156-953-6

ALIGNMENTS

Alignment Scores:	2.865-94
Score:	880.50
Percent Similarity:	70.7%
Best Local Similarity:	53.9%
Query Match:	52.2%
DB:	12
Gaps:	1

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	880.5	52.2	2862	12	US-11-156-953-6
2	880.5	52.2	4716	12	US-11-156-953-6
3	418.5	27.3	1363	9	US-11-077-619-51
4	418.5	24.8	969	12	US-11-074-176-193

Sequence 4, Application US/11156953
 ; Application No. US2006003051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cleary, Joseph
 ; Coleman, Russell
 ; Hardling, Nancy
 ; Pacelli, Yamin
 ; TITLE OF INVENTION: GENETICALLY PURIFIED GELLAN GUM
 ; FILE REFERENCE: 012047 00029
 ; CURRENT APPLICATION NUMBER: US/11/156,953
 ; CURRENT FILING DATE: 2005-06-20
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 4716
 TYPE: DNA
 ORGANISM: Sphingomonas elodea
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1591) ... (3450)
 US-11-156-953-4

Alignment Scores:
 Pred. No.: 5.39e-94 Length: 4716
 Score: 880.50 Matches: 173
 Percent Similarity: 70.7% Conservative: 54
 Best Local Similarity: 53.9% Mismatches: 89
 Query Match: 52.2% Indels: 5
 DB: 12 Gaps: 12

US-09-390-846-2 (1-330) x US-11-156-953-4 (1-4716)

Qy 9 ArgProlysLeAlaMetvaIgylSerGlyMetIleGlyIlyThrMetAlaPheLeuCys 28
 Db 1881 CGCAAGAAGATCGCTGATGGCTCCGGATGTCGGCACCTCGGCACCTCGCT 1940
 Qy 29 SerLeuArgGluLenglyAspvaIvalLeuLeuAspValValProAsnMetProMetGly 48
 Db 1941 GCAATCAGGAACATGGGATCATCGGATCGCTGTGACATCGAGGAGCGAGGGC 2000
 Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValtryGly 68
 Db 2001 AAGGCCCTCGACATCCACAGTCGGACACTCGAACCTCGTCAAGGGCT 2060
 Qy 69 SerAsnSertryGluCysLeuLysGlyAlaAspValIleLeuLeuAspIleLeuCys 88
 Db 2061 GGAAACGCTACGAGACATGGGCGCCACGTCATCGTACCGCCGTTATCCCG 2120
 Qy 89 LysIleProGlyLyssSerAspIleGlyItrpSerAspMetAspLeuLeuProValAsnIle 108
 Db 2121 CGCAAGCGGGC-----ATGGCCGGGAcAtCtCAGACCAACCTG 2165
 Qy 109 LysIleMetArgGluValGlyIyaAlaAlaIleIleSertryCysProAsnAlaPheValIle 128
 Db 2166 GGCGTGATGAGGCCCTGGGAGGGCATCCCGCCACCGGCCGACGGCTTCTGATC 2225
 Qy 129 AsnIleThrAsnProLeuAspValMetValAlaIaLeuGlnGluSerSerGlyLeuPro 148
 Db 2226 TGCATCRAACCCGCTGACGGCATGGTGGGGCTGCGGAGTTCTGGGCTGCG 2285
 Qy 149 HisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMetIle 168
 Db 2286 CACAGAGGCTGTCGCGCATCGCGCTGACTCGGCGCTTCGCACTTCCTC 2345
 Qy 169 AlaAspIleLeuGluValSerProArgIleSerGlyValIleGly 188
 Db 2346 GACACCTGGTCCGGATCGAGATTGACGCCATCCGGCTCGCGACACGGC 2465
 Qy 189 AspHisMetValProLeuSerArgTyraIalThrValAspGlyIleLeuGluIle 208
 Db 2406 GACACCTGGTCCGGATCGAGATTGACGCCATCCGGCTCGCGACACGGC 2465
 Qy 209 ValLysIleGlyItrpIleLysIleGluValAspAspIleValIleThrHrlySval 228
 Db 2466 ATCAAATGGCTGTCACCGGACGCCATCGGCTCGCGACCCGCTG 2525
 Qy 229 AlaGlyGlyGluIleValArgLeuLeuGlyGlySerAlaTyryTralaProGlyAla 248
 Db 2526 GCGGCCGCGAGTCGCGCTGCTAAGACGGCTTATAGCGCCGCCACC 2585
 Qy 249 SerAlaIleGlmMetalGluSertryIleLeuLeuAspArgValMetValCysSer 268
 Db 2586 AGGGCGATGGCATGGGAGGCTATCGAAGGAAAGGCTGCTTCCTGCC 2645
 Qy 269 CystYleGlyGlyGlyGlyIleGluLeuGluAspIleValProCysValIle 288
 Db 2646 GGGACCCACCGCCAGTACGGCTGAGCTGTCGGGCGCCATCGTCATC 2705
 Qy 289 GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuIleGluArgGlnGlu 308
 Db 2706 GCGAAGGGCGGCTGAGCATCGTCAAGGAAACTGGTGCAGTCAGGCTAAGGCC 2825
 Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnIysAlaIleAlaLeuAla 328
 Db 2766 TTGACACTCGCTCGATGCGSTCAAGGAACTGGTGCAGTCAGGCTAAGGCC 2825
 Qy 329 Ser 329
 Db 2826 TCG 2828
 Qy RESULT 2
 US-11-156-953-4

Qy 109 LysIleMetArgGluValAlaIleIleLeuAspSerGlyMetValIleGlyValIleGly 188
 Db 4020 GGCGTCAATGAGGCCGCTGGGAGGCTACCGGCCGACGGGTCTCGTATC 4079
 Qy 149 HisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMetIle 168
 Db 4080 TGCAATACCAACCCGACCATCTCAGACCAACCTGTC 4139
 Qy 149 AspHisMetValProLeuSerArgTyraIalThrValAsnGlyIleProLeuSerGluPhe 208
 Db 4140 CACCAAAGGCTGTCGCGCATGGCCCGCTGTCAGTC 4199
 Qy 169 AlaAspIleGluValSerProArgAspValGlyGlyMetValIleGlyValIleGly 188
 Db 4200 GCGGGAATCAAATGTCGTCGAGCTACCGCCCTCGTGTGCTGGGCAAGCGGC 4259
 Qy 189 AspHisMetValProLeuSerArgTyraIalThrValAsnGlyIleProLeuSerGluPhe 208
 Db 4260 GACACCATGTCGCGTGTGATGAGATTGACCGTGCAGCTGGCCATCCGGACCCGACTG 4319
 Qy 209 ValLysIleGlyGlyItrpIleIleGluValAspAspIleValIleGluValAsp 228

Sequence Comparison Report										
Sequence A		Sequence B		Comparison Results						
Index	Sequence	Index	Sequence	Match		Mismatches		Indels		Gaps
222	AAGTAGCTTAATGCCGGGATCGACCCGAGGCTTCACCGGCTTGTGAAAGCAGTTGTTGCAATTGCTTAATAAAC	281								
31	ArgGluLeuGlyAsp---ValValLeuAspValValProAsnMetProMetGlyLys	49								
282	CGAGGATCACAGATGAGCTTGATGATTGATGTTAATGAGCTGGGAT	341								
50	AlaMetAspIleSerHisAsnSerValValAspThrGlyIle	65								
342	GTGATGGATTACCCACGGAAAGGCTT-----GCGTACACCGTCAAACAA	392								
66	ValThrGlySerAsnSerThrGlyCysLeuLysGlyAlaAspValValIleThrAla	85								
393	TCTTACCGA-----ACATATGAGACTGCAGGAGCTGATATTGCTGCAATTGGCC	446								
86	GlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuPro	105								
447	GGAGCAACCAAAANACCTGGTCA	491								
106	ValAsnIleSerIleMetArgGluValGlyAlaAlaIleLysSerIleCysProAsnAla	125								
492	AAGACTTGAGATTTCAAAAGCATGTTGAGACTCATGCGAGCGGCC	551								
126	PheValIleAsnIleThrAspProLeuAspPheValAlaAlaIleGlnGluSerSer	145								
552	ATTTCTTAGTCGGCAAAATCGGTGATATCCGACTTCAGCACATGCAAATTCAGC	611								
146	GlyLeuProIleHisBargIleCysGlyMetalAlaGlyMetLeuAspSerSerArgPheArg	165								
612	GCCCTGCACAAAGGCGGTATGTTGAGGCGCACACACTGATTCGCAATTGCTCGT	671								
166	ArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGly	185								
672	TTCATGCTGAGCAATTGCGAAATCATTCGGCCTCAAACGTCATATTATGGAA	731								
186	ValHisGlyAspHisMetValProLeuSerArgTyralaThrValAlaGlyIleProLeu	205								
732	GAGCACCGCGCACACAGCTTCCTGTTGGACGCCAGGAATGTCGCCGGCTG	791								
206	SerGlyProIleValLysGly---TrpIleGlyGluValAspAspIleValGln	224								
792	AGTGAATCTCGTGAAGAAACGATGCTGAGAAACGATGCTGAGGAGCTGCACCAAAATTTGAT	851								
225	LysThrLysValAlaGlyGlyGlutLeuArgLeuLeuGlyGlyLysSerAlaTyrr	244								
852	GATGTAAAACGCACTTACATCATGATGAG-----AAAAAGCGGCACTATTATT	905								
245	AlaProGlyAlaSerAlaIleGlnMetAlaGluSerIleLeuGlyAspGlyVal	264								
906	GGGGTGTGCGATGAGCTTGCCTGCAATTACAACGGCCATTCTCATATGAAAACGCTAA	965								
265	MetValCysSerCysTyrLeuGlyGlyGlnGlyIleGlyValGlnAspIleLeuGlyIval	284								
966	TTAACCTCACACATATTGACGCCGCAATACGGTCAAGTCAGTGAATCGGTGT	1021								
285	ProCysValleGlyGlyArgGlyValGluLysIleLeuGluLeuThrAlaGln	304								
1026	CCGGCTGTCGAAATGCGGAAAGGAACTGCGAGCTATCATGCTGAGCTAAATGAA	1081								
305	GluArgGlyLeuGlySerIleAspLysGluMetCinLys	321								
1086	GAAAGAAGAACAGTTCTTCAGCGCGCTCCCTAAACATTTAAA	1136								
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US-11-074-176-193										
; Sequence 193, Application US/11074176										
; Publication No. US20050250135A1										
; GENERAL INFORMATION:										
; APPLICANT: Klaenhammer, Todd R.										
; ATTORNEY: Russell, William M.										
; APPLICANT: Altermann, Eric										
; APPLICANT: McAllife, Olivia										
; APPLICANT: Andrea Azcarate										
; SEQ ID NO: 51										
; LENGTH: 1363										
; TYPE: DNA										
; ORGANISM: Bacillus subtilis										
; FEATURE: gene										
; LOCATION: (1)..(1363)										
; OTHER INFORMATION: 1dh										
; FEATURE: CDS										
; NAME/KEY: CDS										
; LOCATION: (201)..(1166)										
; PRIORITY FILING DATE: 2002-09-11										
; SOFTWARE: PatentIn version 3.3										
; SEQ ID NO: 51										
; LENGTH: 1363										
; TYPE: DNA										
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; LOCATION: (1166)..(1363)										
; PRIORITY FILING DATE: 2002-09-11										
; SOFTWARE: PatentIn version 3.3										
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; NAME/KEY: CDS										
; LOCATION: (1363)..(1666)										
; PRIORITY FILING DATE: 2002-09-11										
; SOFTWARE: PatentIn version 3.3										
; SEQ ID NO: 51										
; LENGTH: 1363										
; TYPE: DNA										
; ORGANISM: Escherichia coli										
; FEATURE: CDS										
; NAME/KEY: CDS										
; LOCATION: (1666)..(1966)										
; PRIORITY FILING DATE: 2002-09-11										
; SOFTWARE: PatentIn version 3.3										
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; FEATURE: CDS										
; NAME/KEY: CDS										
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; SOFTWARE: PatentIn version 3.3										
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; PRIORITY FILING DATE: 2002-09-11										
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; NAME/KEY: CDS										
; LOCATION: (2866)..(3166)										
; PRIORITY FILING DATE: 2002-09-11										

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Stress-Related Proteins and Uses Thereof
FILE REFERENCE: 5051-634
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SEQ ID NO: 193
LENGTH: 969
TYPE: DNA
ORGANISM: *Lactobacillus acidophilus*
FEATURE:
NAME/KEY: CDS
LOCATION: (1) . . . (969)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0) . . . (0)
OTHER INFORMATION: ORF 271; L-lactate dehydrogenase; L-LDH
US-11-074-176-193

Alignment Scores:
Pred. No.: 1.04e-39 Length: 969
Score: 418.50 Matches: 101
Percent Similarity: 56.3% Conservative: 83
Best Local Similarity: 30.9% Mismatches: 124
Query Match: 24.8% Indels: 19
DB: 12 Gaps: 10

US-09-390-846-2 (1-330) x US-11-074-176-193 (1-969)

Qy 1 MetAlaValPheGluLysAsnThrArgProlysIleAlaMetValGlySerGlyMetIle 20
Db 1 ATGCCAAGACTGTAATAACCTCGT-----AAAGTTATTATTTAGTTGTGACGGTGTCTGTA 54

Qy 21 GlyGlyThrMetAlaPheLeuCysSerIleuArgGluIleGly-----AspValVal 37
Db 55 GGTTCTACTTTGCAATT 108

Qy 38 LeuPheAspValValProAspMetProMetGlyLysAlaMetAspIleSerHisAsnSer 57
Db 109 ATCATTTGATTTCTAAGGAAACAGTTACCGCAATGACTTAGCA---GATGCT 165

Qy 58 SerValAlaSpnThrGlyIlePheValValTyrGlySerAlaSerTyrGlyIleGly 77
Db 166 ACTCCATGACATTTCCTAACAGAACATTTACCGCAATGACTGTCAGTCAGTC-----AGGAC 222

Qy 78 AlaAspValValIleIleThrAlaGlyIleThrLysIleProGlyLysSerAspIysGlu 97
Db 223 GCGACTGATGACTTATCTACTGCTGCTCACAAAGCCAGGTTGA----- 270

Qy 98 TrpSerArgMetAspIleLeuProValAsnIleLysIleMetArgGlu---ValGlyAla 116
Db 271 --ACTCTGCTGACCTGTTAACAAAGACTTACATCATCTGTTGACCA 327

Qy 117 AlaIleLeuSerTyrCysProAsnAlaPheValIleAsnIleThrAlaProLeuAspAla 136
Db 328 GRTGTTGATCAGCTTGAAAGTTATCTCTTAGTA--GTTGCTAACCCACTGACATC 384

Qy 137 MetValAlaAlaLeuGlnIleSerIleLeuProHisIleSargIleCysGlyMetAla 156
Db 385 TTTACTCAGCGACTTGDAAGTTACCTGCTTCAGGATGCGCTTACGGATGCTGAGGT 444

Qy 157 GlyMetLeuAspSerSerArgPheArgMetAlaIleAspIysLeuGluValSerPro 176
Db 445 ACTTCACCTGATCATGCTGTCATGCTCAAAAGGTATGCTAAATGGAAACCTTGACCA 504

Qy 177 ArgAspValGlnIleMetValIleGlyValIleGlyIleSphisMetValProLeuSerArg 196
Db 505 CGTCAGTTAATGCATACATGCTGGTAAACACGGTGTACTGAAATCCCAACTATGAGGC 564

Qy 197 TyrAlaThrValAsnGlyIleProLeuSerGluPheValIleGlyTrpIleGln 216

Db 565 TACACAATCTTGGCCCTAAACGTTACCGACTGGTTAAGGCTCACCGTATGGATGAA 624
Qy 217 GluGluValAspIleValGlyIleSphrLysValAlaGlyGlyGluIleValGlyLeu 236
Db 625 TCTAAGCTGAAAGAACATCCACAGGAAGTGTGCTGACATGGCTTAAGACATTATCACAC--- 681
Qy 237 LeuGlyGlyIleSerAlaIleGlySerAlaIleGlySerAlaIleGlySerAlaIleGly 256
Db 682 ---AGAAGGGTGTCACTCTAGGTATGGTAAGCTCAGAAATGATGCTGTAAGGT 738
Qy 257 TyrIleLysBspArgPheArgLysArgValMetValCysSerCysTyrLeuGlnGlyGly 276
Db 739 ATCTGAAACGATGACACCTGACTTCACACTCTGCAATGATGCTACGGT 798
Qy 277 ValGlnAsnIleIleGlyIleValProCysValIleGlyIleArgGlyIleValGlyIle 296
Db 799 TTACAGCACCTTCACATTGCTACCTCTGCAAGTTGTTGGCCGTAACGGTCCTGAACT 858
Qy 297 IleGluLeuIleGluIleThrAlaGlnIleArgGlnIleLeuIleGlySerIleAspGluVal 316
Db 859 ATTGAATGCTTACCGTGATAAACAGCTAAGCTTCTGCTAAGGAAATT 918
Qy 317 LysGlu---MetGlnIysIle 322
Db 919 AAGGAAGTTATGGACAAAGCC 939
RESULT 5
US-10-947-249-109
Sequence 109, Application US/10947249
Publication No. US2005287941A1
GENERAL INFORMATION:
APPLICANT: Akira NAKAGAWARA
APPLICANT: Mikio OHIRA
APPLICANT: Shin ISHII
APPLICANT: Takeshi GOTO
APPLICANT: Hiroyuki KUBO
APPLICANT: Takahiro HIRATA
APPLICANT: Yasuko YOSHIDA
APPLICANT: Saichi YAMADA
TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Meth
FILE REFERENCE: 117007
CURRENT APPLICATION NUMBER: US/10/947,249
PRIORITY APPLICATION NUMBER: US 60/505,614
PRIORITY APPLICATION NUMBER: 2003-09-25
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 1661
TYPE: DNA
ORGANISM: Homo sapiens
US-10-947-249-109
Alignment Scores:
Pred. No.: 3.71e-38 Length: 1661
Score: 408.00 Matches: 102
Percent Similarity: 53.6% Conservative: 71
Best Local Similarity: 31.6% Mismatches: 138
Query Match: 24.2% Indels: 12
DB: 8 Gaps: 7
US-09-390-846-2 (1-330) x US-10-947-249-109 (1-1661)
Qy 5 GluIysAsnThrArgProlySileAlaMetValGlySerGlyMetIleGlyGlyThrMet 24
Db 143 GAACAGACCCCCCAGATAAGATTACAGTTGCGGTGCTGCTGATGGCTGT 202
Qy 25 AlaPheLeuCysSerIleArgGluIleGlyIleAsp---ValValLeuPheAspIvalValPro 43
Db 203 GCCATCAGTATCTTAAATGCAATGCTGGTAAACACGGTGTACTGAACTGACTGGCAGATGAAAGCTTGTGATGTCATGAA 262
Qy

PRIOR FILING DATE: 2003-12-01
 NUMBER OF SEQ ID NOS: 1596
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 1061
 LENGTH: 1661
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial sequences:primer
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1661)
 OTHER INFORMATION: lactate dehydrogenase a (LDHA) gene.
 US-11-000-688-1061

Alignment scores:
 Pedi. No.: 3.71e-38 Length: 1661
 Score: 408.00 Matches: 102
 Percent Similarity: 53.6% Mismatches: 138
 Best Local Similarity: 31.6% Indels: 12
 Query Match: 24.2% Gaps: 7

US-09-390-846-2 (1-330) x US-11-000-688-1061 (1-1661)

Qy 5 GluLy**s**AsnThrArgProlysIleAlaMetValGlySerGlyMetIleGlyGlyThrMet 24
 Db 143 GAACAGACCCCCCAAGATAAAGATTACAGTCTGGCATGGCTGTGCTTGGCTTGCTGT 202

Qy 25 AlaphLeucy**s**SerIleutArgLluLeuglyAsp--ValValLepheAspValValPro 43
 Db 203 GGCATCAGTATCTTAATGAAAGACTTGGCAGATGAACTrGCTCTGTGATGTATCGAA 262

Qy 44 AsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGly 63
 Db 263 GACAATTGANGGGAGATGATGGATCTCAAACAGGCCCTTCCTTAGAACACCA 322

Qy 64 IleThrValtyrGlySerAsnSerIleutArgLluLeuglyAlaAspValValIleIle 83
 Db 323 AAGATITGTCCTGGCAAAGAC---TATAATGCTRACTCTGCAAACTCCAGCTGTCTATTTC 379

Qy 84 ThrAlaGly**y**IlethrLysIleProGlyLysSerAlysGluTrpSerArgMetAspLeu 103
 Db 380 AGCGCTGGGACCGTACAGAACAGGGAGAA-----AGCCGCTCTTAATTG 424

Qy 104 LeuProValAlaIleMetArgGluValGlyAlaAlaIleLysSerTyrCysPro 123
 Db 425 GTCCACCGTAACGIGACATATTAAATTCACTCATCATTCCTATGTGTTAAAATACGCCG 484

Qy 124 AsnAlaPheValleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlu 143
 Db 485 AACTGCAAGTCCTATTGTTCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 484

Qy 144 SerSerglyLeuProHisIleArgLluLeuglyAlaAlaIleGluValGlyMetGln 320
 Db 545 ATAATGGTGTTCCTCCAAAACCGTGTATGGGACTGTTGGGAGTAACTGGATTAGGGAT 604

Qy 164 PheArgArgMetIleAlaAspIleSerCysTyrlLeuGlnGlyLysValGlnAsnHis-- 280
 Db 605 TTCCGGTACCTGATGGGAAAGGGTCTTGGGAAAGGGTCTTGGGAAAGGGTCTTGGG 664

Qy 184 IleGlyvalHisGlyAspHisMetValProLeuSerArgTyrlAlaThrValAsnGlyile 203
 Db 665 CTTGGGGAAACATGGAGATTCCAGTCTGGCTGATGGCTGATGGCTGATGGCTGATGG 724

Qy 204 ProLeuSerGluPhe--ValValIleGlyTrpIleGlyGluValAspAspIle 222
 Db 725 TCTGGAAACTCTGCACCCAGATTGGGACTGAACTGAACTGGTCTTGGTCTTGGTCTTGG 724

Qy 223 ValGlnIleGlyValAlaIleGly--GluIleValAargLeuIleGlyGly 241
 Db 785 GTTCACAGCAGGTGGTTGAGAGTGTCTGATGGGTGATCAACTCAAGGGTACACATCC 844

Qy 242 AlaTyrrTyraAlaProGlyAlaserAlaIleGlnMetAlaGlyserIleutLysAspArg 261
 Db 845 -----TGGGTATTGCACTCTGTAGCATGTTGGAGATATAAGGATCTT 898

Qy 262 LysArgValMetValyCysSerCysTyrlLeuGlnGlyLysValGlnAsnHis-- 280
 Db 899 AGGGGCTGCACCCAGTTCCACCATTAAGGGCTCTTAAGGAAATAAGGATGATGTC 958

Qy 281 TyrLeuGlyValProCysValIleGlyArgGlyIvaAgluLysIleGluLeuGlu 300
 Db 959 TTCCCTTAGTGTCTCTGCAATTGGGACAGAATGGATCTAGACCTTGGCAAGGTGACT 1018

Qy 301 LeuThrAlaGlyGluArgGlyGluLeuGlnGlySerIleAspGluValLysGluMetGln 320
 Db 1019 CTGACTCTGAGGAAGAGGCCGTTGAAGAGTCAGATACTTGGGGATCAA 1078

Qy 321 LysAlaIle 323
 Db 1079 AAGGAGCTG 1087

RESULT 6
 US-11-000-688-1061
 Sequence 1061, Application US/11000688
 Publication No. US200502875441
 GENERAL INFORMATION:
 APPLICANT: BERTUCCI, Francois
 APPLICANT: HOULGATE, Remi
 APPLICANT: BIRNBAUM, Daniel
 TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
 FILE REFERENCE: 1423-4-03
 CURRENT APPLICATION NUMBER: US/11/000, 688
 CURRENT FILING DATE: 2004-12-01
 PRIOR APPLICATION NUMBER: US 60/525,987
 223 ValGlnLysThrLysValAlaGlyGly--GluIleValArgLeuGlyGlnGlySer 241
 785 GTTCACAAAGCAGGTTGAGTGTAGGAGTCTTGTAGGAGTCAAACAGTGGAAAGAG 844

Qy 242 AlaTyr-TyrAlaProGlyAlaSerAlaLeuGlnMetAlaGluSerTyrLeuLysAspArg 261
 Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 845 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 ---- TGGCTTATGGACTCTGTAGCAATTGGAGATTTGCAATTGGAGATAAAGAAATCT 898
 ; Sequence 92, Application US/10955054A
 ; Publication No. US2005066420A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PUSZTAI, LAJOS
 ; APPLICANT: SYMMANS, W. FRASER
 ; APPLICANT: HESS, KENNETH R.
 ; APPLICANT: AYERS, MARK
 ; APPLICANT: STEC, JAMES
 ; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
 ; FILE REFERENCE: UTXC:880US
 ; CURRENT APPLICATION NUMBER: US/10/955,054A
 ; NUMBER OF SEQ ID NOS: 195
 ; SEQ ID NO: 92
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-955-054A-92

Alignment Scores:
 Pred. No.: 4.87e-38 Length: 1336
 Score: 4.06.00 Matches: 99
 Percent Similarity: 51.5% Conservative: 75
 Best Local Similarity: 29.3% Mismatches: 130
 Query Match: 24.1% Indels: 34
 DB: 8 Gaps: 10

RESULT 8
 US-10-947-249-93
 ; Sequence 93, Application US/10947249
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YANADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; PRIORITY APPLICATION NUMBER: 2003-09-25
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 93
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

Qy 5 GluLysAnthrArgPro-----LysIleAlaMetValGlySerGlyMetIleGlyGly 22
 Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 145 GARAGGCCAACAGTCACCTCCAAACATAAGATCACTGGTAGTGGCTTGCACAA 201
 ; Sequence 94, Application US/10947249
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YANADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; PRIORITY APPLICATION NUMBER: 2003-09-25
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 94
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

Qy 202 -----ATGGCGTGCTCATCGCTTTCGGAAAAGTCCTCTGGGTGATGAACTCTGCT 252
 ; Sequence 95, Application US/10947249
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YANADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; PRIORITY APPLICATION NUMBER: 2003-09-25
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 95
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

Qy 23 ThrMetAlaPheLeuCysSerLeuGluIleGlyGly-----AspValAla 37
 ; Sequence 96, Application US/10947249
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YANADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; PRIORITY APPLICATION NUMBER: 2003-09-25
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 96
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

Qy 38 LeuPheAspPvalValProAsnMetProMetGlyLysAlaMetAspIleSerIleAsnSer 57
 ; Sequence 97, Application US/10947249
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YANADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; PRIORITY APPLICATION NUMBER: 2003-09-25
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 97
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

Qy 253 CTTGTGGATGTTGGAGATAAGCTTAAGGAGAAATGCTTGTGGCTTGTGGCTGCG 312
 ; Sequence 98, Application US/10947249
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YANADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; PRIORITY APPLICATION NUMBER: 2003-09-25
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 98
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-947-249-93
Alignment Scores:
 Pred. No.: 4.87e-38 Length: 1336
 Score: 406.00 Matches: 99
 Percent Similarity: 51.5% Conservative: 75
 Best Local Similarity: 29.3% Mismatches: 130
 Query Match: 24.1% Indels: 34
 DB: 8 Gaps: 10

US-09-390-846-2 (1-330) x US-10-947-249-93 (1-1336)

Qy 5 GluLysAsnThrArgPro----LyIleAlaMetValGlySerGlyMetIleGlyGly 22
 Db 145 GAAAGGCCAACAGTCCAACATADRAGTCACGTAGCTGGTGTTGCAAGTTGT--- 201
 Qy 23 ThrMetAlaPheLeuCysSerLeuArgGluLeuGly----AspValVal 37
 Db 202 -----ArgCGTrNGCTATCAGCATTCCTGGAAAGTCAGTACTGGTGTTGCAAGTTGT---
 Qy 38 LeuPheAspValProAsnMetPromeGlyLysAlaMetAspIleSerHisAsnSer 57
 Db 253 CTTGTCGATGTTGAAAGATAAAGCTTAAGGAAATGATGATCGCACCATGGAGC 312
 Qy 58 SerValAspPheGlyIleThrValIrrValtryGlySerAsnSertryGluCysLeuLysGly 77
 Db 313 TTATTCCTCAGACCT---AAAATGTCGAGATAAAGATTAATCTGTACCGCAAT 369

Qy 78 AlaAspValValIleThrAlaGlyIleThrLysIleProGlyLysSerAspIleGlu 97
 Db 370 TCTAAAGTTGTAAGTGTAGCTGGTAACTCAGGAGTCCTCGTAGAACAGGGAG----- 417

Qy 98 TrpSerArgMetAspIleLeuProValAsnIleLysIleMetArgGluValGlyAlaAla 117
 Db 418 ---AGTCGGCTCAATCTGGAGAGAAATGTCATATTCTGTACCGCAAT 474

Qy 118 IleLysSertryCysProAsnAlaPheValIleThrAsnProLeuAspIleGlu 137
 Db 475 ATCGTCAGTAGCTCACGTCCTGATGTCATATAATTGCTGTTCCACCGTGACATTCT 534

Qy 138 ValAlaAlaLeuGlnGluUserGlyLeuProHisHisArgIleCysGlyMetAlaGly 157
 Db 535 ACGTATCTTACCTGGAAACATAAGTGGATTAACCAAAACACCGGTGATTGGAGTGT 594

Qy 158 MetLeuAspSerSerArgPheArgAGMetIleAlaAspIleLeuGluValSerProArg 177
 Db 595 AATCTGGATTCTGGCTAGATTGGCTACATTGGCTGAANAAACTTGGCATCCAGC 654

Qy 178 AspValIglnGlyMetValIleGlyIleProLeuSerArgTyr 197
 Db 655 AGCTGCCATTGGATGGATTGGGGAACTGCGACTCAAGTGGCTGTTGGACTGGT 714

Qy 198 AlaThrValAsnGlyIleProLeuSerGluPhe-----Val 209
 Db 715 GTGAATGGCAAGGTGTTCTCCAGGAATTCAGAAATGGGAACATGACAATGAT 774

Qy 210 LysLysGlyTcPheIleGlySerGluValAspAspIleValGlnLysThrLysValAla 229
 Db 775 AGTGAATAATTTGG-----AAGGAAGTGCATAAGATGGCTGAAAGTGCCAT----- 822

Qy 230 GlyGlyGluIleValArgLeuGlyIleSerAlaItyrTyrAlaProGlyAlaSer 249
 Db 823 -----GAGTCATCAAGCTA-----AAAGGATATAACACACTGGTTATGGATAAGT 870

Qy 250 AlaIleGlnMetAlaGluUsertryLeuLysAspArgLysArgValMetValCysserCys 269
 Db 871 GGGCTGATCTTATGAACTGTTCAAARATCTACTCAGGATTCCATCGGTGAAACA 930

Qy 270 TyrLeuGlnGlyGlnItyrGlyValGlnAsnHis---TyLeuGlyValProCysValIle 288
 Db 931 ATGGTAAAGGGGATCTATGAGATGAAGTCCTGGCATTCAGCTTCCATGTTCTC 990

Qy 289 GlyGlyArgGlyValGluLysIleGluLeuGluLeuThrAlaGluGlnGlu 308

Db 991 AATGCCCGGGGATTAAACCAGGGTTATCAAGGATGAGCTAAGGATGCTGCTAG 1050
 Qy 309 LeuGlyGlySerIleLeuGlySerGluValValGlySerGlyMetGlnIysAlaIleAlaLeu 326
 Db 1051 CTCAAGAAAAGTCAGTACCTGGACATCCAGAGCTAACAGAGCTAACAGACTAACAGCTG 1104

RESULT 9
 US-10-506-443A-1
 ; Sequence 1, Application US-10506443A
 ; Publication No. US10506443A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sahin Dr., Ugur
 ; INVENTOR: Tureci Dr., Ozlem
 ; ATTORNEY: Koslowski Dr., Michael
 ; TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use There
 ; FILE REFERENCE: 342-39CT
 ; CURRENT APPLICATION NUMBER: US-10/506, 443A
 ; CURRENT FILING DATE: 2004-09-01
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1171
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-506-443A-1

Alignment Scores:
 Pred. No.: 5.43e-38
 Score: 405.00
 Percent Similarity: 52.9%
 Best Local Similarity: 30.9%
 Query Match: 24.0%
 DB: 7
 Gaps: 7

US-09-390-846-2 (1-330) x US-10-506-443A-1 (1-1171)

Qy 5 GluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMet 24
 Db 104 GATGAAAACCTCCAGTGTAAATTACTATTGTTGGAACTGTGCGCTAGGGATGGCTGT 163

Qy 25 AlanpheLeuCysSerLeuA9GluLeuGlyAsp----ValValLepheAspIleValPro 43
 Db 164 GCTATPAGTATCTTACTGAAAGATTGGCTGATGAACTTGCCCTGATGATGTTGCTGATG 223

Qy 44 AsnMetProMetProMetGlySAlaMetAspIleSerHisAsnSerValValAspIleGly 63
 Db 224 GACAACACTGAAAGGAAANGATGGATCTTCAGCTGGCATGCTCTTCTTAGTCATCA 283

Qy 64 IleThrValtyrGlySerAsnSerItyrGluCysLeuLysGlyAlaAspValValIleIle 83
 Db 284 AAGATTAICCTCTGGAAAAAGT----TACAGCTCATGCAAACACTCCAGAAATGTTGTC 340

Qy 84 ThraIaglyIleThrLysIleProGlyLysSerAspIleGluIleSerArgMetAspLeu 103
 Db 341 ACAGCAGGTGCAAGGAGCAGCAGGGAAAGAA-----ACTCGCTTGCCTCTG 385

Qy 104 LeuProValAlnIleLysIleMetArgGluValGlyAlaAlaIleLysSertryCysPro 123
 Db 386 GTCCAACTGTAATGIGCTATATGAAATCATCATTCCTGCAATGTCATTATGCTCT 445

Qy 124 AsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlu 143
 Qy 446 GATTGTAAAATCTCTGTTGTTCAAAATCCACTGAAATTTGACTATATAATGTCGGAAAG 505

Qy 144 SerSerGlyLeuProHisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArg 163
 Db 506 ATAAGTGGCTTACCTGTAACCTGTTAATGGAACTGTTAATGCTGCTGCGCT 565

Qy 164 PheAspArgMetIleAlaAspIleGluValIleSerProArgAspValGlnGlyMetVal 183
 Db 566 TTCCGTTACCTAATGGAGAAAATGGTCCACCCACAAGGTTGCTCATGGCATGGTGGATT 625

Qy

Qy 184 IleGlyValHisGlyAspHisMetValProLeuSerArgTyraAlaThrValAsnGlyIle 203
 Db 626 ATTGGAAACATGGTGTCTAGTCGSCCTATGGACTGGCGCTGCTGTT 685

Qy 204 ProLeu---SerGluPheValLeuAspGlyTrpIleLys 215
 Db 686 GCTCTGAAGACTGGACCTAAATTAGAACGGATCAGATAAGGAACTGG---- 739

Qy 216 GluGluGluValAspAspIleValGlyIleSerIleValAlaGlyGlyIleValArg 235
 Db 740 -----AAAAATCCATAAACAGTTATTCAAGTGCCPATGAATTACAG 787

Qy 236 LeuLeuGlyGlnGlySealatTyrrTyrrAlaProGlyAlaSerAlaIleGlnMetAlaGlu 255
 Db 788 CTGAAAGCCGTATACCTC---TGCGCTATTGGACTCTGCTGATGACTGGTAGGA 841

Qy 256 SerTyrlleuIleAspArgLysArgValMetValCysSerCysTyrlleuGlnGlyGlnTyrr 275
 Db 8412 TCCATTGAAAAAATCTTAGGAGTAGGACCTGGACCTGGTAAAGGGATTAT 901

Qy 276 GlyValGlnGlyAspDnsHis---TyrLeuGlyValProCysValIleGlyGlyArgGlyValGlu 294
 Db 902 GGATAAAGAAAGAAACTCTTCAGATCCCTGTCTCTGGCGGGAAATGGTGTCTCA 961

Qy 295 LysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlySerIleAsp 314
 Db 962 GATGTTGCGGAAATTAACTGAAATTCTGAAAGGAGGCCCTTTCAAGAAGGTGCAA 1021

Qy 315 GluVallysGluMetGlnIlys 321
 Db 1022 ACACTTGCGAATTCAGAAAG 1042

RESULT 10
 US-10-793-626-1411
 ; Sequence 1411, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU1480US
 ; CURRENT APPLICATION NUMBER: US/10/793_626
 ; PRIORITY APPLICATION NUMBER: 2004-01-04
 ; PRIORITY FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 1411
 ; LENGTH: 969
 ; TYPE: DNA
 ; FEATURES:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 ; US-10-793-626-1411

Alignment Scores:
 Pred. No.: 1.12e-37 Length: 969
 Score: 401.50 Matches: 93
 Percent Similarity: 53.0% Conservative: 75
 Best Local Similarity: 29.3% Mismatches: 140
 Query Match: 23.8% Indels: 9
 DB: 8 Gaps: 4

RESULT 11
 US-10-793-626-2383
 ; Sequence 2383, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU1480US
 ; CURRENT APPLICATION NUMBER: US/10/793_626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIORITY APPLICATION NUMBER: 60/164,258
 ; PRIORITY FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2383
 ; LENGTH: 969
 ; TYPE: DNA

Qy 11 LysIleAlaMetValGlySerGlyMetIleGlyGlyIleGlyThrMetAlaPheLeuCysSerLeu 30
 Db 37 AAAGTTGTTTACTAGGGAGCGTTCCCTAGGTCAAGTTGCTATGGTCACT 96

Qy 31 ArgGluLeuGlyAsp---ValValLeuPheAspValValProAsnMetProMetGlyLys 49
 Db 97 CAAGGAATGGAGATGATGTAATTGTTGTAATTGATATTGCAAAAGATAAAATGGAAAGCACAGAC 156

;

;

;

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence: synthetic

OTHER INFORMATION: nucleic acid sequence

US-10-793-626-2383

Alignment Scores:

Pred. No.:	Length:	969
Score:	Matches:	93
Percent Similarity:	Conservative:	75
Best Local Similarity:	Mismatches:	140
Query Match:	Indels:	9
DB:	Gaps:	4

US-09-390-846-2 (1-330) x US-10-793-626-2383 (1-969)

Qy 11 LysIleAlaMetValGlySerGlyMetIleGlyGlyIleGlyIleLeuCysSerLeu 30

Db 37 AAAGTTGGTTAGGGAGCTTCAGGTTCAGTTATGCATTTGCTATGGACT 96

Qy 31 ArgGluLeuGlyAsp--ValValLeuPheAspValValProAsnMetProMetGlyLys 49

Db 97 CAAGGAATTGACATGATTGTAATTGATATTGATAATTGAAAGTGGAAAGCCAGAC 156

Qy 50 AlaMetAspIleserHisAsnSerValValAspIleGlyIleLeuValTyrGlySer 69

Db 157 GTAAAGTTAACCATGGCACTTACAGTTCTACCAGTGACTGTA--AAAGCT 213

Qy 70 AsnSerTyrGlycSerLeuIleGlyAlaAspValValIleLeuThrAlaGlyIleThrLys 89

Db 214 GGAAATATGAAAGATTGAAAGTGTGACATTAGTTACAGGTTCACCTCAA 273

Qy 90 IleProGlyLysSerAspLysSerGluTrpSerArgMetAspLeuProValAsnIleLys 109

Db 274 AAACCGGGTGAA-----ACTCGTTTACAACTTGTTGAGAAAATACTAAA 318

Qy 110 IleMetArgGluValGlyAlaAlaIleLysSerTyrGlySerAsnAlaPheValLeuAsn 129

Db 319 ATCATGAAGATCTGTAACTAGTGTCTGGATAGTGGCTTGTATGGTTCTCCDATT 378

Qy 130 IleIleAlanProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyIleLeuProHis 149

Db 379 GCTGCAAACCCAGTTGATCATCTAACCGTTGATCTAACAGGTATGGTTAACAGAGTTACCGACT 438

Qy 150 HisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIleAla 169

Db 439 GAACGTTGATTCGTTCTGGTACAGTGTCTGGATAGTGGAAAGTTCAAGTATTAATAGT 498

Qy 170 AspDysLeuGluValSerProArgAspValGlyMetValIleGlyValIleGlyAsp 189

Db 499 AAGAATTAAGGTTTACCTCAAGTAGTGTCTACGCTAACATTAGGTGAACATGGTAC 558

Qy 190 HisMetValProLeuSerArgTyrAlaLthrValAsnGlyIleProLeuSerGluPheVal 209

Db 559 TCTGAACTTGCACTTGTCTCAAGCAMACGTTGGASCTATTCACTGTTACATG 618

Qy 210 LysLysGlyTrpIleLysGlnGluValAspAspIleValGlnIleThrValAla 229

Db 619 AAGAAGAAACTCTGGATGCTAACCGTAAAGCTAACATTATAACAGAGATGCT 678

Qy 230 GlyGlyGluIleValAlaLeuGlyGlnGlySerAlaTyrAlaProGlyAlaSer 249

Db 679 GCTTACGTTACATCA-----GCTAAGGATCTAGGTATTATGCTATGCTCTAGCA 732

Qy 250 AlanLeGlnMetAlaGluSerTyrLeuIleAspArgIysArgValMetValCysSerCys 269

Db 733 CTATTACCTTCTAACGCTTACTAAATAATGAAATAATGTTGACACTTTCTAGT 792

Qy 270 TyrLeuGlnGlyGlnTyrGlyValGlnAsnHistYLeuGlyValProCysValIleGly 289

Db 793 CAACTTAATGGCAATATGGATTAAACGGATGTTATCTGGTTACCAACACTATCAT 852

Qy 290 GlyArgGlyValGluLysIleGluLeuGluLeuGluArgGlnGluLeu 309

Db 853 CAAATGTCGAGTAAATTGATAACCCATTAAATGATAACGGACTACAATTCA 912

Qy 310 GlyGlySerIleAspGluValGlySerGlyMetGlnLysAlaAlaAlaLeu 326

Db 913 GAAAATCAGTGAAGAACCTTGTAGAGCACCTATGATTCATAAAACATTA 963

RESULT 12

US-10-793-626-4355/c

Sequence 4355, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PUS480US

CURRENT APPLICATION NUMBER: US/10/793-626

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 4355

LENGTH: 3019

TYPE: DNA

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: nucleic acid sequence

US-10-793-626-4355

Alignment Scores:

Pred. No.:	Length:	3019
Score:	Matches:	93
Percent Similarity:	Conservative:	75
Best Local Similarity:	Mismatches:	140
Query Match:	Indels:	9
DB:	Gaps:	4

US-09-390-846-2 (1-330) x US-10-793-626-4355 (1-3019)

Qy 11 LysIleAlaMetValGlySerGlyMetIleGlyGlyIleGlyIleLeuCysSerLeu 30

Db 1791 AAAGTTGTTTGTAGGAGACGGTTCGTTCAAGTTAGCTATGGTCACT 1732

Qy 31 ArgGluLeuGlyAsp---ValValLeuPheAspValValProAsnNetProMetGlyLys 49

Db 1731 CAAGGAAATTGAGATGAATTGTAATTATGATGTCAGATGAAAGATAAAGTGGAAAGCAGAC 1677

Qy 50 AlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGlySer 69

Db 1671 GTTAAGATTAAACCATGGTCACCTTACAGTTCTACAGGTGACTGTA--AAAGCT 1615

Qy 70 AsnSerTyrGluCysLeuIleGlyAlaAlaIleLysSerValIleThrAlaGlyIleThrLys 89

Db 1614 GGAGATAATGAGATGCTAAAGTCAGCATTTAGTGTGTTATTACAGGTTGACCTCAA 1555

Qy 90 IleProGlyLysSerAspLysGluTrpSerArgMetAspLeuProValAsnIleLys 109

Db 1554 AAACCGGGTGAA-----ACTCGTTTACACTGTTGAGAAAATACTAAA 1510

Qy 110 IleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValLeuAsn 129

Db 1509 ATCATGAAAGTTACATGGTCACCTTACAGTTCTACAGTGTGACTCTCTCAATT 1450

Qy 130 IleIleAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuProHis 149

Db 1449 GCTGCAAACCCAGTTGATCTAACGCTTAAACGCTTGTGTTAAAGAGTACAGGTTTACAGCT 1390

Qy 150 HisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPhaHArgArgMetIleAla 169

Db 1389 GAACGCTGTTATGGTTCTGGTACAGGCTCATAGTGGCAAGATTGATTTAAAGT 1330

Qy 170 AspLysLeuGluValGlyValGluIleValAspLeuGlyMetValIleGlyAsp 189

1329 AAAGAATTGGTTACATCAAGTAGTGTGTTACCGCTAGCATTATAAGTGAAACATGGAC 1270
 Db 1225 GTAAAGATTAACCATGETGCACCTTACAGTCTTACCAAGTGACTA--AAAGCTA-- 1281
 Qy 190 HisMetValProLeuSerArgTyAlaThrValAspGlyIleProLeuSerGluPheVal 209
 Db 1269 TCTGAACTTGCACTGGTTGGCTCAAGCAAACGTGTTAGGTATTCTAGTGTATCACATG 1210
 Qy 210 LysLysGlyTrpIleGlyGlnGluValAspDilevalGlnIleThrLysValAla 229
 Db 1209 AAAGAAGAAACTGGTAGCTAACGGATGATGAAATTATAAGAGATGCT 1150
 Qy 230 GlyGlyGluIleValArgLeuGlyGlySerAlaTyrrTyRAlaProGlyAlaSer 249
 Db 1149 GCTTACCATATCATTCAGTATTGTTAGCTCTAGCA 1096
 Qy 250 AlaIleGlnMetAlaGluSerTyLeuIleBspAtpGlySerGly 269
 Db 1095 CTATTACGTATTCTAAAGCTTACTAAATAATGATTGAGTTGACGTTCTAGT 1036
 Qy 270 TyrLysGlyGlnIrrGlyvalGlnAsnHistTyLeuGlyValProGlyValGly 289
 Db 1035 CAACTAAATGGCAATTAGGATTAACTGGCTTACCAACATTAATCAAT 976
 Qy 290 GlyArgGlyValGlyIleGluLeuGluLeuThrAlaGlnGluLeu 309
 Db 975 CAAATGTCGCAAGTTAAATTATGAAACCACTTAAATGATAACATTTA 916
 Qy 310 GlnglySerIleAspGluValIysGluMetGlnLysAlaIleAlaLeu 326
 Db 915 GAAAATCAGTAAAAACTTTAGAAGACACTATGATTCTAAACATTTA 865

RESULT 13
 US-10-793-626-3793
 ; Sequence 3793, Application US/10/793626
 ; PUBLICATION NO. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEAR ACIDS AND PROTEINS
 ; FILE REFERENCE: P1348015
 ; CURRENT APPLICATION NUMBER: US/10/793, 626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3793
 ; LENGTH: 4093
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-3793

Alignment Scores:
 Pred. No.: 6.98e-37 Length: 4093
 Score: 401.50 Matches: 93
 Percent Similarity: 53.0% Conservative: 75
 Best Local Similarity: 29.3% Mismatches: 140
 Query Match: 23.8% Indels: 9
 DB: 8 Gaps: 4

US-09-390-846-2 (1-330) X US-10-793-626-3793 (1-4093)

Qy 11 LysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCysserLeu 30
 Db 1105 AAATGTTGTTGAGGACGCTGGTAGGTCAAGTTATGCTATGGTGTACT 1164

Qy 31 ArgGluLeuGlyAsp--ValValLeuPheAspValValProAspMetProMetGlyLys 49
 Db 1165 CAGGAATGGCAGATGAAATTGTAATTGATTCGCAAAAGATAAAGTGGAAAGCAC 1224

Qy 50 AlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValtyrGlySer 69

RESULT 14
 US-11-128-061-676
 ; Sequence 676, Application US/11/128061.
 ; PUBLICATION NO. US20060003958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Melville, Mark W.
 ; APPLICANT: Charlebois, Timothy S.
 ; APPLICANT: Mounts, William M.
 ; APPLICANT: Hamm, Louane E.
 ; APPLICANT: Sinafore, Martin S.
 ; APPLICANT: Leonardi, Mark W.
 ; APPLICANT: Brown, Eugene L.
 ; APPLICANT: Miller, Christopher P.
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
 ; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
 ; FILE REFERENCE: 01997-027701
 ; CURRENT APPLICATION NUMBER: US/11/128, 061
 ; CURRENT FILING DATE: 2005-05-11

PRIOR APPLICATION NUMBER: US 60/570,425
 PRIORITY FILING DATE: 2004-05-11
 NUMBER OF SEQ ID NOS: 7285
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 1376
 LENGTH: 1317
 TYPE: DNA
 ORGANISM: Cricetinae gen. sp.
 US-11-128-061-676

Alignment Scores:
 Pred. No.: 7.48e-37
 Score: 396.00
 Percent Similarity: 52.3%
 Best Local Similarity: 31.2%
 Query Match: 23.5%
 DB: 12

US-09-390-846-2 (1-330) x US-11-128-061-676 (1-1317)

Qy 5 GluLysAsnThrArgProValLeuAlaMetAlaValGlySerGlyMetIleGlyGlyLysGlyThrMet 24
 Db 92 GATAAAACCTCCGGTAAAGAACATGTCAGCATGGGAGATGGCATGGCT 151

Qy 25 AlaPhaLeuCysSerLeuArgGluLeuGlyAsp---ValValLeuPheAspValValPro 43
 Db 152 GCTATTAGTATCTTACAGAAAGATTGGCCGTGAACCTGGCTTGTTGACACTGATAACC 211

Qy 44 AsnMetProMetLysLysAlaMetAspLiesSerHisAsnSerValValAspThrGly 63
 Db 212 GCAAACGTGAAGGGAGAACGCTGGATCTTCGATGCCAGTCCTTCTCAACACTCA 271

Qy 64 IleThrValtyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIle 83
 Db 272 AGATTGCTCTGAAAGAT---TACAGTGTCTGCACAAATTAGTTATCATC 328

Qy 84 ThrAlaGlyIleThrLysIleProGlyLysSerAspLysLeuGlyAspValVal 103
 Db 329 ACAGCCGGCTGCTAGGGAGAAGGGGGAA-----ACAGCCCTGACTG 373

Qy 104 LeuProValAsnLysIleMetArgGluValGlyAlaAlaAlaLysSerTyrCysPro 123
 Db 374 GTCCAGGGCTAACCTGGCTATCATGAAATCCATGTTCTGGCTTAGTCACAATAGTCCT 433

Qy 124 AsnAlaPheValLeuAsnProLeuAspValMetValaAlaLeuGluGlu 143
 Db 434 GACTCTAAATGTTGTCATGAACTCGCAGATTTTGATCTGTTGCTGAAAG 493

Qy 144 SerSerGlyLeuProHisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArg 163
 Db 494 ATAAGGGCCCTCTGAAACTCGTAACTGGAGTCGCTTAACCTGAGATTCGCCGT 553

Qy 164 PheArgArgMetIleAlaAspLysLeuAspSerProAspValGlnAlaMetVal 183
 Db 554 TTTCGCTTACTGTTGATTCGAGAGAATGTTGCTGTCACCCCTACAAAGTTGCCACCTGCGCTT 613

Qy 184 IleGlyValIleGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIle 203
 Db 614 CTGGAGAACACGGTCACTGAACCCAGGGACTCAGACCAAGGCAACTGGAAAG 733

Qy 204 ProLeu-----SerGluIleValGlyIleValGlyIleValArg 215
 Db 674 CTTCTGAACTGACTGAACCCAGGGACTCAGACCAAGGCAACTGGAAAG 733

Qy 216 GluGluGluValAspAspIleValGlyIleValGlyIleValArg 235
 Db 734 -----ATCCACAAACCAAGCTGGTGGAGAGCTGGCTATGGTTCTCCGG 775

Qy 236 LeuLeuGlyGlySerAlaTyrrTyrAlaProGlyAlaSerAlaLeuGluMetAlaGlu 255
 Db 776 CTGAAAGGGCTTACATCT-----TGGCTTATGGCTGACAGATCTGGCAGAA 829

Qy 256 SerTyrLeuLysAspArgLysSerCysSerCysSerValCysSerValCysSerValCysSerCys 275

Db 830 TCAATCTGAGAAATCTTAGGGGTTGCACTCCGTTAACCTGGTTAAGGGCTTAT 889
 Qy 276 GlyValGlnAsnHis---TyrLeuGlyValProCysValLeuGlyGlyLysArgGlyValGlu 294
 Db 890 GAGATAAGGAAAGAAATCTTCAGCATTCCTTATCTGGACAAAAGGCTMCACA 949
 Qy 295 LysIleIleGluLeuGluLeuThrAlaGlnGluLeuGlnGlySerIleAsp 314
 Db 950 GACATTGTGAAAGTGAACCTGAATCCGAGGAGGCCCTCTCGGAAGAGTGGGAA 1009
 RESULT 15
 US-11-128-049-676
 Sequence 676, Application US/11128049
 Publication No. US20060010513A1
 GENERAL INFORMATION:
 ; APPLICANT: Melville, Mark W.
 ; APPLICANT: Charlesbois, Timothy S.
 ; APPLICANT: Mounts, William M.
 ; APPLICANT: Haun, Louane E.
 ; APPLICANT: Leonard, Martin S.
 ; APPLICANT: Brown, Eugene L.
 ; APPLICANT: Miller, Christopher P.
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METABOLISM
 ; TITLE OF INVENTION: MAKING AND USING SAME
 ; FILE REFERENCE: 01987-027700
 ; CURRENT APPLICATION NUMBER: US/11-128,049
 ; CURRENT FILING DATE: 2005-05-11
 ; PRIOR APPLICATION NUMBER: US 60/570,425
 ; NUMBER OF SEQ ID NOS: 7285
 ; SEQ ID NO: 676
 ; SOFTWARE: Patentin version 3.3
 ; PRIORITY FILING DATE: 2004-05-11
 ; LENGTH: 1317
 ; TYPE: DNA
 ; ORGANISM: Cricetinae gen. sp.
 US-11-128-049-676
 Alignment Scores:
 Pred. No.: 7.48e-37 Length: 1317
 Score: 396.00 Matches: 102
 Percent Similarity: 52.3% Conservative: 69
 Best Local Similarity: 31.2% Mismatches: 132
 Query Match: 23.5% Indels: 24
 DB: 12 Gaps: 7
 US-09-390-846-2 (1-330) x US-11-128-049-676 (1-1317)
 Qy 5 GluLysAsnThrArgProValLeuAlaMetValGlySerGlyMetIleGlyGlyThrMet 24
 Db 92 GATAAAACCTCCGGTAAAGAACATGTCAGCATGGGAGATGGCATGGCT 151
 Qy 25 AlaPhaLeuCysSerLeuArgGluLeuGlyAsp---ValValLeuPheAspValValPro 43
 Db 152 GCTATTAGTATCTTACAGAAAGATTGGCCGTGAACCTGGCTTGTTGACACTGATAACC 211
 Qy 44 AsnMetProMetLysLysAlaMetAspLiesSerHisAsnSerValValAspThrGly 63
 Db 212 GCAAACGTGAAGGGAGAACGCTGGATCTTCGATGCCAGTCCTTCTCAACACTCA 271
 Qy 64 IleThrValtyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIle 83
 Db 272 AGATTGCTCTGAAAGAT---TACAGTGTCTGCACAAATTAGTTATCATC 328
 Qy 84 ThrAlaGlyIleThrLysIleProGlyLysSerAspLysLeuGlyAsp---ValValLeuPheAspVal 103
 Db 329 ACAGCCGGCTGCTAGGGAGAAGGGGGAA-----ACAGCCCTGACTG 373
 Qy 104 LeuProValAsnLysIleMetArgGluValGlyAlaAlaAlaLysSerTyrCysPro 123
 Db 374 GTCCAGGGCTAACCTGGCTATCATGAAATCCATGTTCTGGCTTAGTCACAATAGTCCT 433
 Qy 124 AsnAlaPheValLeuAsnProLeuAspValMetValaAlaLeuGluGlu 143
 Db 434 GACTCTAAATGTTGTCATGAACTCGCAGATTTTGATCTGTTGAAAG 493
 Qy 144 SerSerGlyLeuProHisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArg 163
 Db 494 ATAAGGGCCCTCTGAAACTCGTAACTGGAGTCGCTTAACCTGAGATTCGCCGT 553
 Qy 164 PheArgArgMetIleAlaAspLysLeuAspSerProAspValGlnAlaMetVal 183
 Db 554 TTTCGCTTACTGTTGATTCGAGAGAATGTTGCTGTCACCCCTACAAAGTTGCCACCTGCGCTT 613
 Qy 184 IleGlyValIleGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIle 203
 Db 614 CTGGAGAACACGGTCACTGAACCCAGGGACTCAGACCAAGGCAACTGGAAAG 733
 Qy 204 ProLeu-----SerGluIleValGlyIleValGlyIleValArg 215
 Db 674 CTTCTGAACTGACTGAACCCAGGGACTCAGACCAAGGCAACTGGAAAG 733
 Qy 216 GluGluGluValAspAspIleValGlyIleValGlyIleValArg 235
 Db 734 -----ATCCACAAACCAAGCTGGTGGAGAGCTGGCTATGGTTCTCCGG 775
 Qy 236 LeuLeuGlyGlySerAlaTyrrTyrAlaProGlyAlaSerAlaLeuGluMetAlaGlu 255
 Db 776 CTGAAAGGGCTTACATCT-----TGGCTTATGGCTGACAGATCTGGCAGAA 829
 Qy 256 SerTyrLeuLysAspArgLysSerCysSerCysSerValCysSerValCysSerCys 275
 Db 329 ACAGCCGGCTGCTAGGGAGAAGGGGGAA-----ACAGCCCTGACCTG 373

Qy 104 LeuProValAsnIleTyrIleMetArgGluValGlyAlaAlaIleTyrCysSerPro 123
 Db 374 GTCCAGGGTAACTGTCTCATGATGAAATCCATCGTTCCTGCCTTGATGACATACTCT 433
 Qy 124 AsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlu 143
 Db 434 GACTGTAAATGCTGATGCTCTCAAACCACTGGATATTGACTTATGTTGCTGGAAAG 493
 Qy 144 SerSerGlyLeuProLysIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArg 163
 Db 494 ATAAGTCGCCCTGCTGCAACTCGTGTAAATGGAAGTCGGCTGTAACCTAGATCTGCCGT 553
 Qy 164 PheArgArgMetIleAlaAspIleLeuGluValSerProArgAspValGlyMetVal 183
 Db 554 TTCCGGTACTGTTGAGTGGAGATGTTGGTGTGGTCCACCCATCAAGTGCACGGCTGGTT 613
 Qy 184 IleGlyValIleGlyAspIleMetValProLeuSerArgTyrAlaThrValAsnGlyIle 203
 Db 614 CTGGGAAACACGGTAGCTAGTGTGCCCTATGGAGTGTGTGAACTGTTGCTGGCTCGTA 673
 Qy 204 ProLeu-----SerGluPheValIleSlysGlyTyrIleIys 215
 Db 674 CTTCTGAAGTCACTGAAACCCAGCGGTTAGGAAGCGACTCAGGCCAAGGACTCTGGAAAAG 733
 Qy 216 GluGluIleValAspIleLeuGlnLysThrLysValAlaGlyGlyIleValArg 235
 Db 734 -----ATCCACACCAGTGGTSGAGTGCTGATGGCTATGAGTGTCTCCGG 775
 Qy 236 LeuLeuGlySerAlaItyItyValProGlyAlaSerAlaIleGlnMetAlaGlu 255
 Db 776 CTGAAAGGGCTATACTCT-----TGGCTATGGGCTGTCGTGAAAGATGGCAAGA 829
 Qy 256 SerTyrIleAspArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyr 275
 Db 830 TCAATCTGAAAGATCTAGGGGGCATCCGTRTCACACTGTTAACGGCTTATAT 889
 Qy 276 GlyValGlnIleHis---TyrLeuGlyValProCysValIleGlyArgGlyValGlu 294
 Db 890 GAGATAGGGAGAAATCTTCTAGATTCAGTTCTGTTGAAAGGGCATCACA 949
 Qy 295 LysIleIleGluIleGluLeuThrAlaGlnGluArgGlnGluIleGlySerIleAsp 314
 Db 950 GACATCTGAAAGTGAACCTGAACTGATCCGGAGGGCCCTCTAGAAAGTGGAA 1009
 Qy 315 GluValIysGluMetGlnIys 321
 Db 1010 ACACTCCTGGAACGTCCTAAAG 1030

Search completed: March 3, 2006, 01:04:55
 Job time : 418 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 23:58:53 ; Search time 207 Seconds
(without alignments)

2833.794 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVFEKNTRKIAMVGSGMI.....GSTIDEVKEMOKAIAALDASK 330

Scoring table: BL05M62

Xgapext 10.0 , Ygapext 0.5
Ygapext 10.0 , Ygapext 0.5
Fgapext 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSWEB/spool/[US09390846/runat 02032006 104236 4927/app_query.fasta_1
-DB=ISSUED_Patent-NA_QMFT_Fastap_SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cddi
-LIST=45 -DOCAALIGN=200 -THR SCORE=90 -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT_PDO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 XGAPOP=10 -XGAPEXT=0.5 -DEOPT=7
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEOPT=6 -DELEXT=7
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RESULT 1

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-DEOPT=6 -DELEXT=7
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2: /cgn2_6/_pcodata/1/ina/5.COMB.seq:*
3: /cgn2_6/_pcodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/_pcodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/_pcodata/1/ina/6H.COMB.seq:*
6: /cgn2_6/_pcodata/1/ina/PCTUS.COMB.seq:*
7: /cgn2_6/_pcodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/_pcodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/_pcodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1688	100.0	1679	3	US-09-676-882-1	Sequence 1, Appli
2	1034.5	61.3	1785	3	US-09-21-393B-311	Sequence 311, App
3	1034.5	61.3	1785	3	US-09-21-393B-313	Sequence 313, App
4	831.5	49.3	951	6	PCT-US94-037196-1	Sequence 1, Appli
5	706	41.8	1912	2	US-08-270-033B-1	Sequence 1, Appli
6	706	41.8	1912	2	US-08-338-418-1	Sequence 1, Appli
7	694	41.1	870	3	US-09-002-340-6244	Sequence 6244, Ap
C 8	694	41.1	1634	3	US-09-902-540-341	Sequence 341, App
9	641	38.0	978	3	US-09-134-001C-2696	Sequence 2696, Ap

ALIGNMENTS

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US-09-676-882-1
; Sequence 1, Application US/08676882
; Patient No. 6100241
; GENERAL INFORMATION:
; APPLICANT: Koen Johannes
; APPLICANT: van den Boogaart Paul
; APPLICANT: Vermeulen, Arnoldus Nicolaas
; TITLE OF INVENTION: Coccidiosis Poultry vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Akzo No. 6100241el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676-882
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 514
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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SEQUENCE CHARACTERISTICS:
  LENGTH: 1679 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
  MOLECULE TYPE: cDNA to mRNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  ORIGINAL SOURCE:
    ORGANISM: Emilia acervulina
    DEVELOPMENTAL STAGE: Schizont
    IMMEDIATE SOURCE:
      CLONE: EASC2_1
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 280..11269
      OTHER INFORMATION: /function= "Eimeria lactate
      OTHER INFORMATION: dehydrogenase"
    FEATURE:
      NAME/KEY: misc_feature
      LOCATION: 1..51
      OTHER INFORMATION: /label= pBluescriptII
    FEATURE:
      NAME/KEY: misc_feature
      LOCATION: 1624..1679
      OTHER INFORMATION: /label= pBluescriptII
    FEATURE:
      NAME/KEY: misc_feature
      LOCATION: 45..54
      OTHER INFORMATION: /label= EcoRI-linker
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      NAME/KEY: misc_feature
      LOCATION: 1621..1630
      OTHER INFORMATION: /label= EcoRI-linker
US-08-676-882-1

Alignment Scores:
Pred. No.:          4 -41e-197          Length:          1
Score:           1688.00          Matches:          3
Percent Similarity: 100.0%          Conservative: 0
Best Local Similarity: 100.0%          Mismatches: 0
Query Match:       100.0%          Indels:          0
DB:                  3          Gaps:          0

US-09-390-846-2 (1-330) x US-08-676-882-1 (1-1679)

Qy          1 MetAlaValProAlaIlePheGluLysSerThrArgProLysIleAlaMet
Db          280 ATGGCGGTATACAGTATCCGAAAGATAACGCCCAAGATTGCTATA
Qy          21 GlYGLYIleMetAlaPheLeuCYSerLeuArgGluLeuGluGluGlu
Db          340 GGAGGCCACCATGGCTTCCCTGCGAGGGATAACAGGGAACTCGGAAG
Qy          41 ValValProAsnMetProMetGlyLysAlaMetAspIleSer
Db          400 GTGTACCCAACTACGCCATGGAAAGGGATAAGATAAGATGAGGATATC
Qy          61 AspThrGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db          460 GACACGGGTATACAGTATCCGAAAGATAACGCCCAAGATTGCTATA
Qy          81 ValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db          520 GTATAATTAACGCCAGGGATAACAGGGAACTCGGAAGAGAC
Qy          101 MetAspIleLeuProValProAlaIleIleIleIleIleIleIleIle
Db          580 ATGGATCTATTCTGTGATATAAGATAAGATGAGGATATGAGGAGGTC
Qy          121 TyrCysProAsnAlaPheValIleIleIleIleIleIleIleIle
Db          640 TACTGTCTCTTAATGGAATTGTTAATATACAAATCTCCCTT

```

Qy	141	LenglnGluserSerGlyLeuProHisIshisargIlecyGlyMetalAlaGlyMetLeuAsp	160
Db	700	CITCAAGTGTATCGAACCTCATAGATCTGGGTATGGCTGGATGCTTGAT	759
Qy	161	SerSerArgPheArgArgMetIleAaaAspLysLeuGluValSerProArgAspValGln	180
Db	760	AGCTCTCTTTAGACCTATGATGCTGATAATTAGAAGTCCTAGATGAGTAGACAG	819
Qy	181	GlyMetValIleGlyValHisGlyAspDhiMetVaProLeuSerArgTyRAlaThrVal	200
Db	820	GGATGGTCATAGGTGTACACGGGTACATGGGCCCTTAAGTGAATGATGCACAGTT	879
Qy	201	AsnGlyLleProLeuSerGluheavallyblysGlyTrpIleGlyGluGluValAsp	220
Db	880	AAGGCATCCGGTTCTGAGTTGTTAGAGGGCTGATCAAGGAGAAAGTAGAT	939
Qy	221	AspIleValGlnLysThrLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGly	240
Db	940	GATATGGTTCAGAGACCAAGTGGCTGGAGAGATGTACGCTATTGGACAGGGC	999
Qy	241	SerAlaTyrrTyraIalaproGlyAlaSerAlaIleGlnMetAlaGluSerTyrlLeuWlyAsp	260
Db	1000	TCTGCTCTACTAAGCTCCAGGGCTCTAGCTATTCAATGCTGGCTGAGGCTTAAGGAT	1059
Qy	261	ArgLyGlyArgValMetValCysSerCysTyrlLeuGlnGlyGlnTyryValGlnAnHis	280
Db	1060	AGAAAGACAGTGTATGGTTGCTTGTACTTGCAAGGACAATATGGTACAGATCAC	1119
Qy	281	TyrLeuGlyValProCysValleGlyArgGlyValGluLysIleIleGluLeuGlu	300
Db	1120	TACTTAGAGTACCTTGTTATCGTGGAGGGCTTGAGAGTTATTGAGTAA	1179
Qy	301	LeuThrAlaIleGlnLysGluGlnGlyserIleAspGluVallyGluMetGln	320
Db	1180	TGAGCCGCAAAAGAACAGAGGAGCTCAGGATCATCGTGAAGGTTAAAGAGTCAG	1239
Qy	321	LysAlaIleAlaIleLeuAspAlaSerLys	330
Db	1240	AAGCTTATGGCTCTGTATGCATCCAAAG	1269
RESULT 2			
US-09-216-399B-3:1			
; Sequence 3:1, Application US/09216393B			
; Patent No. 6511694			
; GENERAL INFORMATION:			
; APPLICANT: Milhaugen, Michael James			
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USE			
; FILE REFERENCE: TX-1-C2			
; CURRENT APPLICATION NUMBER: US/09/216,393B			
; CURRENT FILING DATE: 1998-12-18			
; PRIOR APPLICATION NUMBER: 08/994,825			
; PRIOR FILING DATE: 1997-12-19			
; NUMBER OF SEQ ID NOS: 366			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO: 311			
; LENGTH: 1785			
; TYPE: DNA			
; ORGANISM: Toxoplasma gondii			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(75)			
; OTHER INFORMATION: US-09-216-399B-3:1			
Alignment Scores:			
Pred. No. :	1.05e-116	Length:	1785
Score:	1014.50	Matches:	193
Percent Similarity:	77.3%	Conservative:	55
Best Local Similarity:	60.1%	Missmatches:	72
Query Match:	61.3%	Indels:	1
GapS:	1		

US-09-390-846-2 (1-330) x US-09-216-393B-311 (1-1785)	Qy	9 ArgProlysIleAlaMetValGlySerGlyMethylGlyGlySerGlyLeuCys 28
	Db	109 AGAAAGAACGGCCATGATTGGCTCTGGCATGTTGGACTATGGCTACTCTGTC 168
	Qy	29 SerIleArgGluLeuGlyAspValIleUpheAspValValProAlaMetProMetGly 48
	Db	169 GCTTCTCGTGAGCTGCTGACGTGTTCTAGAAGTTGTAAGGTATGCCGGGGT 228
	Qy	49 LysAlaMetAspIleSerHisAnsSerSerValAspThrGlyIleThrValTyrGly 68
	Db	229 AAGCTCTGACCTGAGCCATGAGACCTCGCTGTCACCAACGTTTCGGTCCTGCT 288
	Qy	69 SerIleSerTyrGlu---CysIleUlyGlyAlaAspValValIleIleThrAlaGlyIle 87
	Db	289 GAGTACTCTAACAGGGCGCGCTAACCGGTGGCACTGGCTTATCGTTACCGCCGTC 348
	Qy	88 ThreonylserProGlyIlyserAspIleGlyUrpSerArgMetAspIleLeuProValAsn 107
	Db	349 ACCAAGGTGCCGGCAACCCGACTCCAGTGGAAACGAACTGCTCCGTCAC 408
	Qy	108 IleIleIleMetArgGluValGlyAlaAlaIleIleIleSerTyrCysProAsnAlaIleVal 127
	Db	409 TCGAAGATCATTCGGAGATCGCTAGAACATCAAGAGTACTGCCCAAAGACCTTCAT 468
	Qy	128 IleSerIleIleAsnProIleAspValAlaAlaIleGlyIleSerIleGlyLeu 147
	Db	469 ATCTGGTCACCAACCCGCTGACTGCTATGGTCAAGGTCACTGGAGGGCTCTGGCGTC 528
	Qy	148 ProIleIleIleArgIleCysGlyMetAlaIleGlyIleSerSerArgPheArgArgMet 167
	Db	529 CCGACCAACATGATGATCTGGCTATGGCTCATGTCACAATCTGGCTTCGCAAT 588
	Qy	168 IleAlaAspIleIleGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
	Db	589 GTCGCGCAAGCGCTGCTGCTCCCGCGAGCTCCAGGCCACCTCATGGCACACAC 648
	Qy	188 GlyAsPhi sMetValProIleSerArgTytAlaIleValAnglyIleProLeuSerGlu 207
	Db	649 GGGAACATGCATGTCATGCCCTCGCTTGTGCTGATCATACCGATCAGACTAACGACT 708
	Qy	208 PheIallysLysGlyTrpIleIleGlyIleGluValAspAspIleIleValGlyLysThrLys 227
	Db	709 TTCTCAAGGACCGCTGATGTCAGGAGAGCAGCTCAAGGGATATCTGACACCAAA 768
	Qy	228 ValAlaGlyGlyGluIleValArgLeuGlyGlySerAlaIleTyrAlaProGly 247
	Db	769 GTCCTGCGGCCAGATGTCCTCCCTCGCCAGGTCTCGCTTACTAGCCCCGCC 828
	Qy	248 AlaSerAlaIleGlnMetAlaGluIleSerTyrIleLeuIleAspArgValMetValCys 267
	Db	829 GCATCCGCTGTCGCCATGGCAACATCCCTCTGAAAGCACGAAAGGGCTCATCCCGTGC 888
	Qy	268 SerCystyIleGlyGlnItyrGlyValGlnAsnNHistYrLysGlyValProCysVal 287
	Db	889 AGTTGTACTGCAACGGAGATCGGGCTGTAAGGGACATGTCATGTCCTGGCGC 948
	Qy	288 IleGlyGlyArgGlyValGluIysIleIleGlyLeuGluIaThAlaGinGluArgGln 307
	Db	949 ATGGAGCGCCGGCATGAGCCGGCTCATGAGCTGTCAGGCTGAAAGGGAGAGAAG 1008
	Qy	308 GluIeugGlyIleSerIleAspGluIallysGlyIleSerGlyIleLeuAsp 327
	Db	1009 CGTGTCCGAGAAGTCCTGGCAGACGACTGTCATGGCTCAACGGGGTGTGCTTCAG 1068
	Qy	328 Ala 328
	Db	1069 GCG 1071

Patent No. 6514694
 GENERAL INFORMATION:
 APPLICANT: Milhaugen, Michael James
 TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
 FILE REFERENCE: TX-1-C2
 CURRENT APPLICATION NUMBER: US/09/216,393B
 CURRENT FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 08/994,825
 PRIOR FILING DATE: 1997-12-19
 NUMBER OF SEQ ID NOS: 366
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 313
 LENGTH: 1785
 TYPE: DNA
 ORGANISM: Toxoplasma gondii
 US-09-216-393B-313

Alignment Scores:	
Pred.	No.:
Qy	9 ArgProlysileAlaMetvalGlySerGlyMetileGlyGlyThrMetAlaPheIeuCys
	Length: 1785
Score:	1.05e-116
	Matches: 193
Percent Similarity:	77.3%
	Conservative: 55
Best Local Similarity:	60.1%
	Mismatches: 72
Query Match:	61.3%
	Indels: 1
	Gaps: 1
US-09-390-846-2 (1-330) x US-09-216-393B-313 (1-1785)	
Qy	9 ArgProlysileAlaMetvalGlySerGlyMetileGlyGlyThrMetAlaPheIeuCys 28
Db	109 AGAACAGGGCGCATGATTGCTTGGCATATGGCACTATGGCTACCTGGTC 168
Qy	29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
Db	169 GCTCTCGTGCCTGAGCTGCTGACCTGCTCTAGATGTGTCAAAGGTATGCCGGAGGT 228
Qy	49 LysAlaMetAspIleSerHisAsnSerValValIleAspThrGlyIleThrValTrgGly 68
Db	229 AAGGCTCTTGACCTGCCATGTGACCCATCGTGAACCAACGTTTCGTCGTGCT 288
Qy	69 SerAsnserTyrGlu---CysLeuLysGlyAlaAspValValIleIleThrAlaGlyIle 87
Db	289 GAGTAGCTTACAGGGCGCGTCA CGGTGCGA CTCGGTGTACCGTGTACCGGGTCTG 348
Qy	88 ThrIleAlleProGlyIleSerAspIleAspIleGluTrpSerArgMetAspLeuLeuProValAsn 107
Db	349 ACCAAGCTGCCGGCAAGGCCGACTCGAGTGAGCTGAGAAACGATCTCTCCGCTTCAC 408
Qy	108 IleIleIleMetArgGluValIlyAlaAlaIleIleSerTyrCysProAsnAlaPheVal 127
Db	409 TCGAAATCATTCGGAGATCGTCAAGACATCAAGAAGATACTGCCAAAGACTTCATC 468
Qy	128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluUserSerGlyLeu 147
Db	468 IleAlaAspIysLeuLeuIleValIleSerProArgAspValAlaGlyMetValIleGlyValHs 187
Qy	469 ATCGTGTCAACCCGTGACTGCTGATGGCTCAAGGTCATGGCGAGGCCCTCTGGCTC 528
Qy	148 ProIleHisIleArgGlyMetAlaGlyMetLeuAspSerIleSerIleGlyPheIglnMet 167
Db	529 CGGACCAACATGATCTGGPATGGCTGACTCGTCCGACCTGCTCGTGTGCT 588
Qy	168 IleAlaAspIysLeuLeuIleValIleSerProArgAspValAlaGlyIleProLeuSerGlu 207
Db	649 GGCGACTGCTGGTCCCGTGTGCTCCGGTACATTACCGTAAGCACACTCCCGATCAGARG 708
Qy	208 PheValAlaIleGlyIleLeuIleGlyGluLeuIleAspAspIleValGlnIleIleThrHs 227
Db	709 TTTCATCAAGGAGGCCTAGTCAGGGAAAGCAGCTGAGGAGATGCTGAGCACCCAAA 768
Qy	228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlySerAlaIleIleThrAlaProGly 247

STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 61601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/270,013B
 FILING DATE: 01-JUL-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 FILING DATE: 02-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Robert F.
 REGISTRATION NUMBER: 27555
 REFERENCE/DOCKET NUMBER: 62321
 TELEPHONE: (312) 616-5600
 TELEFAX: (312) 616-5700
 TELEX: (25) 353 3
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1912 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus stearothermophilus*
 STRAIN: ATCC12016
 US-08-270-013B-1

Alignment Scores:
 Pred. No.: 9 ArgProlyleAlaMetValGlySerGlyMetAlaPheLeuCys 28

Score: 2.81e-76 Length: 1912
 Percent Similarity: 706.00 Matches: 140
 Best Local Similarity: 65.9% Conservative: 69
 Query Match: 44.2% Mismatches: 96
 DB: 41.8% Indels: 13
 Gaps: 2

US-09-390-846-2 (1-330) x US-08-270-013B-1 (1-1912)

Qy 9 ArgProlyleAlaMetValGlySerGlyMetAlaPheLeuCys 28
 Db 695 CGAAAAAATCTGGTGTACGGCGATTCAAGGGGACAGCGCTTCCTTRG 754
 Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspV1-----ValProAsnMetPro 46
 Db 755 GCGCAAAGAGCTCGGACCTCGTGTGCGATATCCGCAGTTGAAACCAAAG 814
 Qy 47 MetGlyYsAlaMetAspLeuHisAsnSerSerValAspThrGlyIleThrVal 66
 Db 815 AAAGGGAGGGCCTCGATATGCTCGGCCAGCCCCGTTGCTGGCTTGACGGGATAAC 874
 Qy 67 TyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGly 86
 Db 875 ATCGGCACATCGGATTACGCTGACACGGCGATTCGGACATCGTGTCTCATACAGGAGC 934
 Qy 87 IleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuProVal 106
 Db 935 ATCGCCCGAACGGCGCG-----ATGAGCGCGACGATTCGGTGAACGAGC 979
 Qy 107 AsnIleGlyIleMetArgGluValGlyAlaAlaLysSerTyrGlyProAsnAlaPhe 126
 Db 980 AACCAAAAATTATGAGCAGTGAAGTGTCAAATACTGCCGAACTGCTAC 1039

Qy 127 ValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuClnGluUserSerGly 146
 Db 1040 ATCATGGTCITGACGCCGGTCACTGGATGCGATGACCTATACGGTTAAAGGAATCGGA 1099
 • Qy 147 LeuProIshisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArg 166
 • Db 1100 TTCCCAAAAACCGCTCATGGCACTGGCGCTTGGATACGGCGCTCCGCACT 1159
 Qy 167 MetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyVal 186
 Db 1160 TTCTGGCCGAGGAGTGAACATTGGTAAAGATGTCACTGGTTGTTTAAGCGSC 1219
 Qy 187 HisGlyAspIleAspMetValProLeuSerArgTyrAlaThrValAsnCysIleProLeuUser 206
 Db 1220 CATGGGATGACATGCTGCCCTCGTCGGTACTGACGCCGACATTCGGTCGAA 1279
 Qy 207 GluPheValIleLysGlyIleTrpIleLeuGluValAspAspIleValGlnIleThr 226
 Db 1280 AAACATTCGGAAA-----GATCCTTGTGACGCCATCGTGAAGGGACG 1324
 Qy 227 LysValAlaGlyGlyGluIleValArgLeuGlyGlySerAlaIleTyroIlePro 246
 Db 1325 CGCAAAGGCCGCGCTAACCTGTCACCTGCTGCCAACGGCAGGGCTACTACGCC 1384
 Qy 247 GlyAlaserAlaIleGlyIleValGluIleValGlySerIleGlySerAlaIleTyro 266
 Db 1385 GCCGGCTCGTGTGTCAAATGGTCAAGGATTGAAAGCAGGGCGCATTTGCG 1444
 Qy 267 CysSerCystYrLeuGlyGlyIleGlyIleGlyValGlnAsnHistYrieGlyValProCys 286
 Db 1445 GCGATGGCCPACCTTGCAAGGGAAATACGGCTATGAGGCATTATTGGCGTGC 1504
 Qy 287 ValIleGlyArgGlyArgGlyValGluIleGlyIleGlyLeuIleGluLeuThrAlaGlnGluArg 306
 Db 1505 ATCCCTGGCGCGCAAAGGCATCGAGAAAGTCGAGCTGACCGAAGGAAAGAAAA 1564
 Qy 307 GlnGluLeuGlyIleGlySerIleAspGluIleValGlyMetGlnIleAlaIle 323
 Db 1565 GC-GCCCTCGCCAATTCGGTAAATGTCATGGCATCGT 1614

RESULT 6
 US-08-390-418-1
 ; Sequence 1, Application US/08838418
 ; Patient No. 5744342
 ; GENERAL INFORMATION:
 ; APPLICANT: Sogabe et al.
 ; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALLATE
 ; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 ; STREET: Two Prudential Plaza, Suite 4900
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60601-6780
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,418
 ; FILING DATE: 17-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/270,013
 ; FILING DATE: 01-JUL-1994
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 164701/1993
 ; FILING DATE: 02-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:

Qy 104 LeuProValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysPro 123
 Db 292 CTCGAGATCAACCTGARGATCATGACCGAACGGACGTGGCGGCAACATAGCAGACGCC 351

Qy 124 AsnAlaPheValleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlu 143
 Db 352 AACGCCCTTGTCATCACTGCAACCGCTGGACCCGATGTTGTCGCTCACAG 411

Qy 144 SerSerGlyLeuProHisIleArgGlyAlaAspGlyMetAlaGlyAspGlySerGly 163
 Db 412 ATGCCTGGTCATGCCCAAGCACATGGCTGGCCATGGGCAACCCGGC 471

Qy 164 PheArgArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetAla 183
 Db 472 TTCAAGTGTCTGTCGCGAGGCGCTGGCTCCATCCCAGACTGGCTGAGGCCCTGGT 531

Qy 184 IleGlyValIleGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIle 203
 Db 532 CTGGCCGCCACGGGACATGGTCCGCTGTCGGCAACAGGACGAGCTGGCCGCGTGC 591

Qy 204 ProLeuSerGluPheValIleGlyBglTrpIleLysGlnGluValAspIleVal 223
 Db 592 CCCCTGACGGGAGCTGTCGCAAG-----GRCAAGTGGAGCCATCATC 636

Qy 224 GlnLyserThrIleValAlaGlyGlyGlyIleValArgLeuGlyGlnGlySerAlaTyr 243
 Db 637 AACGGACCCGGAGGGCGCCGGAGCTGTCAGAAGGGAGGGCTAC 696

Qy 244 TyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrIleuLysAspArgLysArg 263
 Db 697 TTGGGGCCCGCGGCGTCGCTGCCATGCGCATGGGAGAGCTTCCTGGAGACGCCAGGC 756

Qy 264 ValMetValCysSerCysteIleGluGlyGlnTyrGlyIleValGlnAsnHsTyrIleuGly 283
 Db 757 GTGCrCCGGCGGCCGCCCTCTGGGGCCAGTAGGGATCAAACGGTACTCTTCGCG 816

Qy 284 ValProCysValIleGlyGlyArgGlyIleValGlyLysIleLeuGluLeu 301
 Db 817 GTCCCCGTTGAGATCGGCGGGCGCGTGTGAGAAGATCCACACGGTGGCTG 870

RESULT 8
 US-09-902-540-341/c
 ; Sequence 341, Application US/09902540
 ; Patent No. 6833447
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiesand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-1015849/B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO: 341
 ; LENGTH: 1634
 ; TYPE: DNA
 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-341

Alignment Scores:
 Pred. No.: 6.52e-75 Length: 1634
 Score: 694.00 Matches: 140
 Percent Similarity: 66.8% Conservative: 59
 Best Local Similarity: 47.0% Mismatches: 87
 Query Match: 41.1% Indels: 12
 DB: 3 Gaps: 3

US-09-390-846-2 (1-330) x US-09-902-540-341 (1-1634)

6 LysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyIleGlyThrMetAla 25
 Qy 866 CAGAATGGCAAGAAGATCGCTCATCGCCGTCAGATCGCGGTCACCTCGCG 807

Qy 26 PheLeuCysserLeuArgGluLeuGlyAspValLeuPheAspVal----ValPro 43
 Db 806 CTGCTCCCGTGCAGAGTGCCTCGTGAACCTGTCGCTGTACGACATCCCGCGGCCGAG 747

Qy 44 AsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerValValAspThrGly 63
 Db 746 GGTCTGGTCAGGGCAAGGCTGGACATACAGCTGACGGTTACGAC 687

Qy 64 IleIleIleValValValValValValValValValValValValValValleIle 83
 Db 686 TGGCGGTGAGGGCACACCGACTGAAAGACGAGCTGAGCTGATCACATC 627

Qy 84 ThrAlaGlyIleThrIleIleProGlyLysSerAspLysGluTrpSerArgMetAspLeu 103
 Db 626 AGCGCCGGCATGCCGCCACCCGCC-----ATGTCGCCGGAGGACCTG 582

Qy 104 LeuProValAsnIleLysIleMetArgLysSerIleValGlyAlaAlaIleLysSerTyrGly 123
 Db 581 CTCGAGATCACCTGAGATCATGGAGCTGGGGCAACATAGCAGCACC GCCCCC 522

Qy 124 AsnAlaPheValleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlu 143
 Db 521 AACGGCTTCGTCATACGNGCCACCCGTCGAGCTGTCGCTCAGCTCACAG 462

Qy 144 SerSerGlyIleProHisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArg 163
 Db 461 ATCGGGGTCTGCCCAGCACATGCCGCCATGCCGCACTGGACACGCCGC 402

Qy 164 PheArgArgMetIleAlaAspLysLeuGluValSerProArgAspValGlyIleVal 183
 Db 401 TTCAAGTGCTTCGTCGCGAGGGCTGGCTCATCCGGGAACTGGAGCCCTGCTGTG 342

Qy 184 IleGlyValIleIleGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIle 203
 Db 341 CTGGGGGCCACGGGAGCATGGTCCCTCTGTCGCAAGAACGAGCTGGGGCTG 341

Qy 204 ProLeuSerGluPheValIleLysIleTrpIleLysGlnGluIleValAspIleVal 223
 Db 281 CCCCTGACGGAGCTCATGGCAAG-----GACAACCTGGCCATCCTAC 237

Qy 224 GlnIleIleThrIleValAlaGlyGlyIleIleValArgLeuLeuGlyGlnGlySerAlaTyr 243
 Db 236 AAGGCCACCCGGTGGGGCCGGCCAGCTGGTGTACAAAGACGGCAGCCCTAC 177

Qy 244 TyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrIleuLysAspArgIleSArg 263
 Db 176 TTGGGCCCCCGGCTGGGAGCTCCCATGGGAGCTCCAGGCTGGGGCTGG 117

Qy 264 ValMetValCysSerCysteIleGluGlyGlnTyrGlyIleValGlnAsnHsTyrIleuGly 283
 Db 116 GTGCTGCCGCCGCCCTCTGGGGCCAGTAGGGATCAACGGTACTTCCTCGGC 57

Qy 284 ValProCysValIleGlyGlyArgGlyIleValGlyLysIleLeuGluLeu 301
 Db 56 GTCCCCGGTGCAGATGGGGGGGGGGGGAGATCCACCCGTCGAGCTG 3

RESULT 9
 US-09-134-001C-2696
 ; Sequence 2696, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 SEQ ID NO 2696
 LENGTH: 978
 TYPE: DNA
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-2696

Alignment Scores:

Pred. No.:	9.37e-69	Length:	978
Score:	64.00	Matches:	132
Percent Similarity:	64.0%	Conservative:	71
Best Local Similarity:	41.6%	Mismatches:	102
Query Match:	38.0%	Indels:	12
DB:	3	Gaps:	4

US-09-390-846-2 (1-330) x US-09-134-001C-2696 (1-978)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrAlaPheLeuCys 28
 Db 46 AGAAAGAAAATGATCATTTATTGGCGGGACATACAGGTGGACTCTGACATTCTT 105
 Qy 29 SerLeuArgGluLeuGlyAbpValLeuPheAsp----ValValProAsnMetPro 46
 Db 106 GCACAAAGGAAATTAGGAGATAATGGTGTGATTGAACTCAGGGCAGCAATCAGGGPATGGCT 165
 Qy 47 MetGlyLysAlaMetAspIleSerHisAsnSerSerValValAlaAspThrGlyIleThrVal 66
 Db 166 AAAGGAAAGCCCTAGATTTAGAAGGACCATATGGGGTTGACACATCTGTA 225
 Qy 67 TyrGlySerAsnSerGlyCysLeuIlysGlyAlaAspValValIleIleThrAlaGly 86
 Db 226 CATGGTCAGTAATATAGAGATAATAAGATTCAAGCATAGTAGTGATGACTSCAGGT 285
 Qy 87 IleThrLysIleProGlyLysSerAspIleProLeuPheAspLeuLeuProVal 106
 Db 286 -----ATACCTAGGAATCAGGA-----ATGACAAGAGAATTAAGGAACT 330
 Qy 107 AsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPhe 126
 Db 331 ATGAAACAATAGTACAGAAATCTGATTAATGCAAGATGTATGCCCTATCAATA 390
 Qy 127 ValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerGly 146
 Db 391 ATTATTCATGCTTGCATTTGATGATCATGTCAGTCAGT 450
 Qy 147 LeuProHisIleArgGlyIleCysProSerSerIleGlyPheArg 166
 Db 451 TTCCCTAAAGAACGTATTATGGTCATCTGAAATTAGAGCTGTCAGATATCGAAC 510
 Qy 167 MetIleAlaAspIleLeuGluValSerProArgAspDvaGlyMetValIleGlyVal 186
 Db 511 TTATTCGTCAGAACTTAACGTGTAATGGTTTTAGGTGA 570
 Qy 187 HisGlyAspHisMetValProLeuSerArgTyrAlaThrValAspGlyIleProLeuSer 206
 Db 571 CATGGTGATCGATGTTAACCTTGATTAATACACACATTAATGGATCCAGTT--- 627
 Qy 207 GluPheValIleLysGlyTrpIleGlnGluValAspIleValGlnLySthr 226
 Db 628 -----AAGCATCTTATTTCTGAAAGAAATGATCAAATTGTAACCTACA 675
 Qy 227 LysValAlaGlyGlyIleValArgLeuGlySerAlaTyrAlaPro 246
 Db 676 CGTAAGGGTGGTCAGAAATTGGCTTACTAGGTCAAGCTAGCATATATGACCA 735
 Qy 247 GlyAlaserAlaIleGlnMetAlaGluSerTyrLeuIysAspArgIleArgValMetVal 266
 Db 736 GCAACTGGTATATACTAGTCATAATTGCAAACTGGTTATTACCA 795
 Qy 267 CysSerCysTYrLeuGlnGlyGlnTyrGlyValGlnAsnHistYleLeuGlyAlaProCys 286
 Db 916 CAACATCACACATCTGGCAACGCTGAGTCAGTCAAACATCA 966

RESULT 10
 US-09-390-846-2
 Sequence 7, Application US/08920812
 Patent No. 5763188

GENERAL INFORMATION:
 APPLICANT: Ohno, Tsuneyuki
 APPLICANT: Matsuhisa, Akio
 APPLICANT: Uehara, Hirotsugu
 APPLICANT: Eida, Soji
 TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 COMPUTER: PC DOS/MS-DOS
 OPERATING SYSTEM: PC DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 APPLICATION NUMBER: US/08/920,812
 FILING DATE: 29-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,577
 FILING DATE: 27-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Rin-Laure, Li-Hsien
 REGISTRATION NUMBER: 33,547
 REFERENCE/DOCKET NUMBER: 19036/32420
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6100
 TELEFAX: 312/474-0448
 TELEX: 25-8856
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5024, base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Staphylococcus epidermidis
 STRAIN: Clinical isolate SE-32
 US-09-390-846-2

Alignment Scores:
 Pred. No.: 1.65e-66 Length: 5024
 Score: 632.00 Matches: 132
 Percent Similarity: 64.2% Conservative: 72
 Best Local Similarity: 41.5% Mismatches: 101
 Query Match: 37.4% Indels: 13
 DB: 2 Query Match: 2 Gaps: 4

US-09-390-846-2 (1-330) x US-09-390-846-2 (1-5024)
 Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
 Db 57 AGAAAGAAAGATCATATACTGGCTGAGTCATCTAGGTCGGACATACAGGGACATACAGGGCATATGCTAGCTTCATTCT 116

29	SerLeuArgGluLeuGlyAspValValLeuPheAsp-----ValValProAsnMetPro	46
30	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
31	117 GCACAAAGGAAATTAGGAAATTTCTGTGATTCAGCCAGCZATCGAGGTATGCCT	176
47	MetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrVal	66
48	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
49	177 AAAAGAAAGCGTAGATATTAGAAGGGACCCATTTGGGGTTTGACACATCTCTGA	236
67	TyrosylSerAsnSerTyrGluCysLeuIlysGlyAlaAspValValIleIleThrAlaGly	86
68	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
69	237 CAGCTTCACTAAATACTAGGAAATTAGAAGATTAAAGCATAGTCGATAGTCAGCTG	296
87	IleThrLysIleProGlyLysSerAspIleGluItpSerArgMet-AspLeuLeuProVa	106
88	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
89	297 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
90	DDB 297 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
91	ATACCTAGAACATTAGAACATTAGCAGAAACTGCAATTACAATTTAGGAAAGATTAGTC	296
106	LasnIleLysIleMetArgGluValGlyAlaAlaAlaIleSerSerTyrCysProAsnAlaP	126
107	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
108	342 TAATGAAACAATAGTACAGAAACTGCAATTACAATTTAGGAAAGATTAGTC	401
126	evalleAarnIleThrAspProLeuAspValMetValAlaAlaIleGluSerSerG	146
127	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
128	402 ARTTATTGCTATTGACTAAATCGGTGTATCATATACAGCATTAAACATCGGG	461
146	YLeuProHisIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArg	166
147	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
148	462 TTRCTCTAAAGAACGTTATTATTGGCAATCTGGATTAGACCTGCAAGATAATCG	521
166	gMetIleAlaAspIleLeuGluValSerProArgAspValGlnGlyMetValIleGly	186
167	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
168	522 TTRATTGCTCAAGAACCTAACGGTCTCTCAARAGATGTAATCGGTTGTTAGGTC	581
186	IHisGlyIaphisMetValProLeuSerArgTyrolylAlaThrValAsnGlyIleProLeu	206
187	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
188	582 ACGGGTGATACTGGTGTACCTTGATTAATAACACACATATGGGTTTCGCTT-	639
206	rGluPheValLysIleGlyTrpIleLysGlnGluGluValAspAspIleValGlnLysR	226
207	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
640	640 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
226	-AGGCATCTTATTCTCAAGAAAAGATTGATCAAATGTGTAAGCT	686
227	rIysValAlaGlyIleGlyGlutLeuValArgIleLeuGlyIleGlySerAlaTyrrAlaP	246
228	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
687	687 ACCGAAAGGTGGTCAGAAATTGTCATTACGGTCAAGGCTCAGCATATAATGCA	746
246	oGlyAlaSerAlaIleGlnMetAlaGluSerItyrLeuIysAspArgLysArgValMetva	266
247	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
747	747 AGCCACTGTATATGAACTATAGATGSCATTTTATGATGAAACGGTTATPTTAC	806
266	266 1CysSerCysteineGlnGlyIleGlyIleGlyIleGlySerItyrLeuGlyValProC	286
267	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
807	807 AAGATTGGTTATAGCGGAGATAACGGTCTGGACTCTCAC	866
286	svallIleGlyGlyArgGlyIleGlyIleIleGluLeuGluSerIleIleGluSerIleIleGlu	306
287	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
867	867 TATAATGAGATATGAGGAATAGGAAAAGATTATGAGGTAGATATGATAATGAGCTA	926
306	9GlnGluIleGluGlnGlySerIleAspGluValLyGluMetGlnIysAlaIle	323
307	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	:
927	927 TCACTACAACTACAACTCTGCCGAGATGTGAGTCAGTCAAACTACACTA	978
Qy	RESULT 11	
Qy	US-08-930-827-7	
Qy	Sequence 7, Application US/08920827	
Ddb	; GENERAL INFORMATION:	
	; APPLICANT: Ohno, Tsuneya	
	; APPLICANT No. 577075	
	; ADDRESS: 1-10-1, Uehara, Hiraotsugu	
	; CITY: Eda, Soji	
	; STATE: Gifu	
	; ZIP CODE: 501-0001	
	; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease	
	; NUMBER OF SEQUENCES: 25	
	; CORRESPONDENCE ADDRESS:	

APPLICANT: Eda, Soji
 TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/920,828
 FILING DATE: 29-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,577
 FILING DATE: 27-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Rin-Laures, Li-Hsien
 REGISTRATION NUMBER: 33,547
 REFERENCE/DOCKET NUMBER: 19036/32420
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEX: 312/474-0448
 TELEX: 25-1856
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5024 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Staphylococcus epidermidis
 STRAIN: Clinical Isolate SE-32
 -08-920-828-7

Alignment Scores:		Sequence Data:			
Aligned No.:	Score:	Length:	Matches:	Conservative:	Mismatches:
1	1.65e-66	5024	5024	132	132
2	632.00	1.32	1.32	72	72
3	64.2%	101	101	101	101
4	BT Local Similarity:	Indels:	Indels:	Gaps:	Gaps:
5	41.5%	37.4%	37.4%	4	4
6	Very Match:	2	2		
7	9	ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAla			
8	57	AGAAGAAAGATATACTATTATGGCGGACATAAGGGGACTCTAGCA			
9	29	SerLeuArgGluLeuGlyAspValValLeuPheAsp-----ValValPro			
10	117	GCACAAAAGGAATTAGGAGTATTCGTGTGATTTGACGCCATTGGGGTTTGAC			
11	47	MetGlyLysAlaMetAspIleSerHisAnsSerSerValValAspThrGly			
12	177	AAAGGAAAGGGCTTGATTTAGAAAGGGGACCCATTGGGGTTTGAC			
13	67	TyrGlySerSerSerTyrGluCysLeuIleGlyAlaAspValValLeu			
14	237	CATGGTTCACTAAATTATAGAGATATTAAAGCTGACATAGTGGTGTGCA			
15	87	IleThrLysIleProGlyLysSerAspLysGluTrpSerArgMet-AspLeu			
16	297	-----ATACCTTAGGAAATTATCGGA-----ATGACAAAGGAAAGATT			
17	106	1AsnIleLysIleMetArgGluIvalGlyAlaAlaAlaLysSerTyrCysPr			

NAME: Arinietto, Pamela Denise
 REGISTRATION NUMBER: 40 489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELEPHONE: (781)833-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 2832:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 975 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (Genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1..975
 SEQUENCE DESCRIPTION: SEQ ID NO: 2832:
 US-09-107-532A-2832

Alignment Scores:

Pred. No.	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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DB:							

US-09-390-846-2 (1-330) x US-09-107-532A-2832 (1-975)

Qy 3 ValPheGluLysAsnThrArgProLeuIleAlaMetValAlySerGlyMetIleGly 22
 Db 25 TTATTCTGAAAAAACAGTCTGTAAGTAGTAATCCGGTACAGTTTGTTGCAACA 84

Qy 23 ThrMetAlaPheLeuCysSerLeuArgGluLeu---GlyAspValValLeuPheAspVal 41
 Db 85 ACTATCCTTAACTAACCAAGTATCACCAAGGAAGCATGGACCTTTAGATGGTATGGCTGGCGAT 144

Qy 42 ValProAsnMetProMetGlyLysAlaMetAspIleSerHISerSerValValAsp 61
 Db 145 AATCAAGAAAAGCAGAAAGGAAAGCATGGACCTTTAGATGGTATGGCTGGCGAT 204

Qy 62 ThrglyIleThrvaltryGlySerAsnSerIleProGlyLysSerAspIleSerValVal 81
 Db 205 GAAATGTGGCTATGG--TCAGGTGGCTATGAAAGATGATGCTGATATCGTT 261

Qy 82 IleIleIleIleAlaGlyIleThrlysIleProGlyLysSerAspIleSerGluTrpSerArgMet 101
 Db 262 GTTATCACGCTGTTAACCAAAACTGCTCAA 306

Qy 102 AspLeuLeuProValAlanylLysIleMetArgGluLysIleAlaIleLysSerIle 121
 Db 307 GATTTTACCTAAAACAATGGCTCAATCATGCCCAAAATCGTAAAGAAATCATGGATCA 366

Qy 122 CysProAsnAlaPheValIleIleAsnIleSerIleAsnProLeuAspValMetValAlaAlaLeu 141
 Db 367 GGATTCCACGGTTATTATCGTTGCTCAAACCCGATGAGATTTGACATATATCGCT 426

Qy 142 GlnGluserSerGlyIleProHisIleSerGlyMetAlaGlyMetLeuAspSer 161
 Db 427 TGGAACGAACTGGCTGCCACATCGCTGTTATCGTACTGGTACGGACAAACATTGGATACA 486

Qy 162 SerArgPheArgArgMetIleAlaAspIleSerProArgAspValGly 181
 Db 487 ACTCGTTTCCGTAAGAAATGCATGAAATTAAAGTGACCTGTCAGTCATGTCACATACACTGCGT 606

Qy 182 MetValIleGlyValHisGlyAspIleMetAlaProIleUserArgIleAlaIleAlan 201
 Db 547 TATATCTTGGAAACATGGTATTAGAACTGGTACATGGTACATGGTACATGTCACATACACTGCGT 606

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/clone="TGSTzyd32a10.y1"
 /dev_stag="tachyzoite"
 /lab_host="DH10B (Genetog, Invitrogen, Inc.)"
 /clone_norm="Norm 7 cDNA Library"
 /note="Vector: pBluscript SK- Site 1: EcoRI; Site 2:
 XbaI; Toxoplasma RH strain tachyzoites were grown in human
 foreskin fibroblast cultures in vitro. The library was
 originally constructed by K.L.Wan, Cambridge University.
 cDNAs were synthesised from polyA RNAs by oligo d(T)
 priming and directionally cloned into the EcoRI site to XbaI
 sites of the Lambda ZapII vector using the ZAP-cDNA
 synthesis kit (Stratagene). The primary cDNA library was
 mass excised as phagemid using Express helper phage
 (Stratagene). Phagemid DNA was extracted by
 phenol-chloroform method, and hybridized against a pool of
 highly abundant genes which were derived from short-cycle
 PCR of the primary cDNA library. The normalized library
 was electroporated into DH10B (GeneHog, Invitrogen, Inc.).
 WARNING: the library contains a small percentage of cDNAs
 derived from the human host cells."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.47e-76 Length: 784
 Score: 742.50 Matches: 140
 Percent Similarity: 77.3% Conservative: 34
 Best Local Similarity: 62.2% Mismatches: 50
 Query Match: 44.0% Indels: 1
 DB: 6 Gaps: 1

US-09-390-846-2 (1-330) x CB025968 (1-784)

Qy 9 ArgProLysLeuAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
 Db 110 AGAAAGAACGGCCATGATTGGCTCTGCATGATGTTGGCACTATGGCTTCACCTGTGTC 169

Qy 29 SerLeuArgGluLeuGlyAspPvalValLeuPheAspPvalValProAsnNetProMetGly 48
 Db 170 GCTCTCCGGAGCTGGCTGAGCTGGCTCTACCATGCTGTCAGCTGTCATAAGGATGCGAGGGT 229

Qy 49 LysAlaMetAspIleSerHisAsnSerSerValIleAspThrGlyIleThrValtryGly 68
 Db 230 AAGGCTTGACCTGACATGACCTCGTGTGACCAAGGTTGCTGCTGCTGCTGCTGCTGCTG 289

Qy 69 SerAsnSerTyrGlu--CysLeuLysGlyAlaaspPvalValIleIleThrAlaGlyIle 87
 Db 290 GAGTACTTACAGGCGCCGGCTACCCGTGCGACATGGTTATGTTACCGCGGTCTGCTGCTG 349

Qy 88 ThriBleProGlyLysSerAspIleAspGluTrpSerArgMetAspLeuLeuProValAsn 107
 Db 350 ACCAGGTCGGGGAAAGGCCGACTCCGGAGCCGAACGTTCTGTCGCCGTCAC 409

Qy 108 IleTyrIleMetArgGluAlaGlyAlaAlaIleIleSerTyrCysProAsnAlaPheVal 127
 Db 410 TCGAGATCATTCGGAGATGGTGAACATAGAAAGTACTGCCAACAGACCTTCATC 469

Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluUserSerGlyLeu 147
 Db 470 ATCGGGTCACCAACCGCTGGACTGATGGTCAAGGTATGTCGACTCTGCGCT 529

Qy 148 ProHisHisArgIleCysGlyMetLeuAspSerSerArgPheArgArgMet 167
 Db 530 CCGACAAATGATGATGTCGCGTATGCCCTCATGTCGACTCTGCGCT 589

Qy 168 IleAlaAspIleGluValSerProArgAspValMetValIleGlyValHis 187
 Db 590 GTGCCGGACGGCTCTGTCCTGCGCTGCGCTGCGCT 649

Qy 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
 Db 650 GGCGACTGATGGTCGCTGCGCTGCGCTGCGCTGCGCT 709

FEATURES
source
 1. .784
 /organism="Toxoplasma gondii"
 /strand="RH" (Type 1)"
 /db_xref="Taxon:5811"

REFERENCE
AUTHORS
 Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M.,
 Clifton, S., Pape, D., Martin, J., Wyliet, T., Dante, M., Marra, M.,
 Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
 Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I.,
 Kennedy, S., Maguire, J., Waterston, R., and Wilson, R.
 Toxoplasma EST Project
 Unpublished (2001)
 Contact: Clinton, S.
 Toxoplasma EST Project
 Washington University School of Medicine
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxo@watson.wustl.edu
 Contact David Sibley (toxoest@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.
 Seq. primer: -40RP from Gibson
 High Quality sequence stop: 440.
 Location/Qualifiers

JOURNAL
COMMENT
 1. .784
 /organism="Toxoplasma gondii"
 /mol_type="mRNA"
 /strand="RH" (Type 1)"
 /db_xref="Taxon:5811"

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Qy	228	ValAlaGlyGlu	232	Db	246	CATATAAGAACCTTCCCTCATGCCTTATCATTGTCGACGAAACCCACTGGACTG	305
Db	770	GTCGCTGGCGCGAG	784	Qy	137	MetValAlaAlaLeuGlnGluSerArgLeuProHisIleArgIleCysGlyMetAla	156
RESULT	4			Db	306	ATGGTGAGTAGTACTCTTCGAGATTGGAGTCCCATAATCATGGATTAAGGT	365
LOCUS	CV637428	CV637428	777 bp	mRNA	linear	EST_01-JAN-2005	
DEFINITION	PVMCH42	Field isolate cDNA library Plasmodium vivax cDNA clone		Qy	157	GLYMetLeuAspSerSerArgPheArgArgMetIleAlaAspLeuGluValserPro	176
ACCESSION	CV637428	CV637428.1	GI:56944246	Db	366	GGTGTGCTAGATACTAGACTGAAATTACATTCGAGAAGTGAACGTCGCCG	425
KEYWORDS	BST	Plasmodium vivax (malaria parasite P. vivax)		Qy	177	ArgAspValGlyGlyMetValIleGlyValIleGlyAspHsMetValProLeuSerArg	196
SOURCE	ORGANISM	Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		Db	426	AGGATGGTTAACATGCCATGTCGACATGGTCTCTGAAAGG	485
REFERENCE	1 (bases 1 to 777)	Carlton, J.M. and Cui, L.		Qy	197	TyrAlaThrValAsnGlyIleProLeuSerGluPheValIleGlyTrpIleLysGln	216
AUTHORS	Unpublished (2004)	Carlton, J.M. and Cui, L.		Db	486	TACATCACAGTGGAGGTATCCATGCCAAAGATTAAACAAAAAGATTACAGAT	545
JOURNAL	Parasite Genomics Group	The Institute for Genomic Research		Qy	217	GluGlyValAspAspIleValGlnIleThrValAlaGlyGlyGluIleValArgLeu	236
COMMENT	The Institute for Genomic Research	9712 Medical Center Drive, Rockville, MD 20850, USA		Db	546	GAGAAGTGGAGGCAATTCGACTGAAACTGTGAACTGTGAGATTGTGAACCTC	605
FEATURES	source	/organism="Plasmodium vivax"		Qy	237	IleGlyGlnGlySerIleAlaTyrrAlaProGlyAlaSerAlaIleGlnMetAlaGluSer	256
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		/strain="Field isolate"		Qy	257	TyrLeuIleAspArgIleSerCysIleThrValAlaGlyGlnItyrGly	276
		/clone="PMCH42"		Db	660	TATTGAGGGATAAAAGAACTGCTGTTGTTCACTCTACTAGGGGCAATCGGC	719
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		/note=vector: Lambda TripleX2		Db	720	CACGACACATCTTGGTACTCTCTCGTATGGGACCCGGATGAGCAA	776
		/note=vector: Lambda TripleX2: Site 1: Sfi 1A; Site 2: Sfi 1B; Plasmodium vivax Field isolate cDNA library made in lambda TripleX2. Inserts cloned unidirectionally produced from pTripleX2 Plasmid. Inserts sequenced from either 5' or 3' end using TripEx2 sequencing primer or polydT 24 bp primer respectively."		RESULT	5		
		/note=vector: Lambda TripleX2: Site 1: Sfi 1A; Site 2: Sfi 1B; Plasmodium vivax Field isolate cDNA library made in lambda TripleX2. Inserts cloned unidirectionally produced from pTripleX2 Plasmid. Inserts sequenced from either 5' or 3' end using TripEx2 sequencing primer or polydT 24 bp primer respectively."		LOCUS	CB025472	753 bp	mRNA linear EST 13-JAN-2003
				DEFINITION	TGES7zyz77h03.y1	TGRH Tachyzoite Norm 5 cDNA Library Toxoplasma Gondii cDNA clone TGES7zyz7h03.y1	5 similar to TR:P90613 P90613
				ACCESSION	CB025472	LACTATE DEHYDROGENASE	,
				VERSION	CB025472.1	GI:27072231	EST.
				SOURCE	Toxoplasma gondii		
				ORGANISM	Toxoplasma gondii		
				COMMENT	Sarcocystidae; Toxoplasma.		
				REFERENCE	1 (bases 1 to 753)		
				AUTHORS	Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tagare, S., Shvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R., and Wilson, R.		
				JOURNAL	Toxoplasma EST Project Unpublished (2001)		
				TITLE	Contact: Clifton, S.		
					Toxoplasma EST Project Washington University School of Medicine		
					4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
					Tel: 314 286 1800		
					Fax: 314 286 1810		
					Email: toxo@watson.wustl.edu		
					Contact David Sibley (toxo@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.		
					Seq. primer: -40RP from Gibco		
					High quality sequence stop: 424.		
					Location/Qualifiers		
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Qy	57	SerSerValValAspThrGlyIleThrValtyrGlySerAsnSerTyrGluCysLeuLys	76				
Db	66	AATGNGATGGCTTATCCATTGAAAGGTGACTGGCTGAACTGTGATGACTGAA	125				
Qy	77	GlyAlaAspValValIleIleThrAlaGlyIleThrValtyrGlySerAspLys	96				
Db	126	GGAGCGAACGGAGATTTACTCCCTGAATGAGATTGAGATTGGGGAAAGCAGAACAG	185				
Qy	97	GlutTrpSerArgMetAspIleLeuProValAsnIleSerArgGluValGlyAla	116				
Db	186	GAATCGAACCGAGATTTACTCCCTGAATGAGATTGGGGAAAGCAGAACAG	245				

/db_xref="taxon:5811"	Qy	208	phevallylysGlyTrpIleLysGlnGluGluValAspAspIleValGlnLysThrIle	227
/clone_stage="Tachyzoite"	Db	685	TTCATCAGGACGGCTGAGTCGGAGATCGCTGAGGAGATCGCTGAGCACCCAA	744
/lab_host="DH10B (Genetix, Invitrogen, Inc.)"	Qy	228	ValAlaGly	230
/clone_lib="TGRH Tachyzoite Norm 5 cDNA Library"	Db	745	GTCGTCGGC	753
/note="Vector: pBluscript SK-, Site 1: EcoRI; Site 2:				
XbaI; Toxoplasma RH strain tachyzoites were grown in human				
foreskin fibroblast cultures in vitro. The library was				
originally constructed by K.L.Wan, Cambridge University.				
cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XbaI sites of the Lambda ZAPII vector using the ZAP-cDNA Synthesis kit (Stratagene). The primary cDNA library was				
mass excised as phagemid using ExAssist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (Invitrogen, Invitrogen, Inc.).				
WARNING: the library contains a small percentage of cDNAs derived from the human host cells."				
ORIGIN				
Alignment Scores:				
Pred. No.:	6.9e-74	Length:	753	
Score:	721.50	Matches:	137	
Percent Similarity:	76.7%	Conservative:	34	
Best Local Similarity:	61.4%	Mismatches:	51	
Query Match:	42.7%	Indels:	1	
DB:	6	Gaps:	1	
US-09-390-846-2 (1-330) × CB025472 (1-753)				
Qy	9 ArgProSleAlaMetAlaGlySerGlyMetIleGlyGlyThrMetAlaPheLeuGly	28		
Db	85 AGAAAGAAAGTGGCATGATTGGCTTGCAATGTTGGACTATGGCTTACCTGTGC	144		
Qy	29 SerIleArgGluIleGlyAspValValPheAspValValProAspMetProMetGly	48		
Db	145 GCTCTCGTGTAGCTGCTGTCAGTCGTCAGTCGTCAGTCGTCAGTCGTCAGTC	204		
Qy	49 LysAlaMetAspIleSerHisAsnSerServAlaThrGlyIleThrValTyros	68		
Db	205 AAGCTCTTGACCTCTGAGCCATGTCAGCTCGTGTGTCAGTCGACACAAACGTTCCGTCGTCGTC	264		
Qy	69 SerAsnSerIleGlu---CysLeuGlyAlaaspValValIleIleAlaGlyIle	87		
Db	265 GAGTACTCTAGGGTCTACCGGTCACGGGACTCGTTATCGTACCGCGCTCG	324		
Qy	.88 ThrLysIleProGlyLysSerAspIleGluTrpSerArgMetAspLeuIeuProValAsn	107		
Db	325 ACCAGGTGCGGGGAAGGCCGACTCGGGCTCGGCTTCAC	384		
Qy	108 IleLysIleMetArgGluValIgylGlyAlaAlaIleLysSerItyCysProAlaPheVal	127		
Db	385 TCGAGATCATTCCGGAGATCGGTCAGAACATCGAGACTACGCCAACCTTCATC	444		
Qy	128 IleAsnIleIleAsnProLeuAspIleValValAlaAlaLeuGluGluSerSerGlyLeu	147		
Db	445 ATCGTGTACCAACCCGGTGTGAGTCAGTGTGAGTCAGTCAGTCAGTCAGTC	504		
Qy	148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMet	167		
Db	505 CGGACCAAATGATCTGCGCTATGCCCTCATGCTGCTGCTGCTGCTGCTG	564		
Qy	168 IleAlaAspIleLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis	187		
Db	565 GTCGGCGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	624		
Qy	188 GlyAspIleAsnIleProLeuSerArgIleValValAlaAlaLeuGlnGluSerSer	207		
Db	625 GGCAACTGGTCCGGTTGTCGGGACATACCGTGAACCGCTACCCGATCAGAG	684		
Qy	208 PheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSer	145		
Db	211 TTATCATGTCGTCAGTGGACAAACCCAGTGGACACTCTCTCTCTGAGCTTC	270		

Qy	146	GlyLeuProIshibargGlyMetCysGlyMetAlaGlyMetLeuAspSerSerAspSerAspPheArg	165	/db_xref="Taxon:5811" /clone="TgGSTzy47c01" /dev_stage="Tachyzoite" /lab_host="Tachyzoite" /note="Vector: pDNR-LIB; Site 1: SfII; Site 2: SfII; The cDNA library was constructed by Kellang Tang, and Robert Cole at Washington University. Total RNA was amplified using SMART cDNA, Clontech Inc.). First strand was PCR amplified using the same primer set and the fragments were digested with SfII. The fragments were size selected, ligated into vector pDNR-LIB containing directional SfII sites, and electroporated into GC10 competent cells. WARNING: the library contains a small percentage of cDNAs derived from the human host cells."
Qy	271	GGAGTCCAAAATAATCATCGATTAGTGCTGTTAGATACTAGTGAA	330	
Qy	166	ArgMetIleGalaAspIleGluValSerProArgAspValGlnGlyMetValIleGly	185	
Qy	331	TATTCATATCGCAGAGTGAACGTCGCCGAGAGTGTAAATGCACATGTCGCT	390	
Qy	186	ValHisGlyAspHisMetValProleuSerArgGlyTyrAlaThrValAsnGlyIleProleu	205	
Qy	391	GCACATGGGACAAGATGTTCTCTGAAGAAAGTACATCACAGTGAGGTATCCCATG	450	
Qy	206	SerGlyIleValValGlyTrpIleGlyGluGluValAspAspIleValGlnLys	225	
Qy	451	CAAGATTATTAAATAACAAAAGATTAAZAGATGAGAGTGGAGGCATTGATGTC	510	
Qy	226	ThrIleValAlaGlyGlyGluIleValArgLeuGlyGlnGlySerAlaTyrTyrAla	245	
Db	511	ACTGTGAAACTGTCTTGGAGATTGAACTCTT-----GCCTCTCTTATGTTGCC	564	
Qy	246	ProGlyAlaSerAlaIleGlnMetAlaGluSerTyLeuLysAspArgIleSarGlyValMet	265	
Qy	565	CCAGGTGCTCCCATCATCAAATGCGGAACTCTTATTTGAGGATATAAAGAAAGTGT	624	
Qy	266	ValCysSerCystYrLeuGlyGlyGlnTrpIleGlyValGlnGlyIleSerGlyValPro	285	US-09-390-846-2 (1-330) x CV551869 (1-684)
Db	625	GTTGTTCTCACTCTACTAGGGCAATATGGGCAATGGCCACAGAACATCTTGTGTTACTCT	684	
Qy	286	CysValIleGlyGlyArgGlyIvaGluValIleGluIleGluLeuIleGlyValGlnGlu	305	
Db	685	CTCGTTATCGGGGACCGAGTGAAGTCACTGACTGAGTCAATGCGTGAATGCGGAGGAG	744	
Qy	306	ArgGlnGluLeuGlyGlySerIleAspGluValAspGluValAspGluValAspGluValAsp	323	
Db	745	AAGACCAGCTTCGACGAGGGAGTGGGAGACTAAAGTAGAGGCGCTCATT	798	
Qy	RESULT	7		
Qy	CV551869			
LOCUS	CV551869	684 bp	mRNA	linear EST 22-OCT-2004
DEFINITION	19ESTRyq47c09.Y3	Tg COUG	Toxoplasma gondii	
	TgESTRyq47c09.Y3	5'	similar to TR-190613 P90613 LACTATE DEHYDROGENASE ; mRNA sequence .	
ACCESSION	CV551869	1	GI:54431926	
VERSION				
KEYWORDS				
ORGANISM	Toxoplasma gondii			
	Bukaryote; Alveolata; Apicomplexa; Coccidia; Bimerida;			
	Sarcocystida; Toxoplasma.			
REFERENCE	1 (bases 1 to 684)			
AUTHORS	Tang,K., Cole,R., Rogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pope,D., Martin,J., Wyllie,T., Dante,M., Marra,M., Biller,L., Kucaba,T., Theising,B., Bowes,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Teagreishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.			
TITLE	Toxoplasma EST Project			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Clifton, S.			
	Washington University School of Medicine Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: toxowatson.wustl.edu			
	Contact David Sibley (toxest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.			
	Seq primer: T7 from Gibco			
	High quality sequence stop: 584.			
	Location/Qualifiers			
	1 .. 684			
	/organism="Toxoplasma gondii"			
	/mol_type="mRNA"			
FEATURES	source			
source	303 AlaGluArgGlnGluLeuGin	310		

9	ArgProlylSerAlaMetValGlySerGlyMetIgGlyThrMetAlaPheLeuCys	28
167	AGAAAGAAGGAAAGAGCTTCCAA	684
RESULT 8		
CB022051	CB022051	772 bp mRNA linear EST 13-JAN-2003
DEFINITION	T9ESTyzy99b11.y1 TGRH Tachyzoite Norm 5 cDNA Library Toxoplasma	
ORGANISM	Gondii cDNA clone T9ESTyzy99b11.y1 5' similar to TR:P90613 P90613	
ACCESION	LACTATE DEHYDROGENASE ; mRNA sequence.	
KEYWORDS	CB022051.1 GI:27692163	
SOURCE	Toxoplasma gondii	
ORGANISM	Toxoplasma gondii	
SARCOPLASMIC RETICULUM	Alveolata; Apicomplexa; Coccidia; Eimeriida;	
REFERENCE	Sarcocystidae; Toxoplasma.	
AUTHORS	Tang,K., Cole,R., Rogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.	
TITLE	Toxoplasma EST Project.	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Clifton, S. Toxoplasma EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: toxo@wuation.wustl.edu Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.	
SEQUENCE	Seq primer: -40bp from Gibco High quality sequence stop: 442.	
LOCATION/QUALIFIERS	Location/Qualifiers 1. dev_stage="Tachyzoite" /organism="Toxoplasma gondii" /mol_type="mRNA" /strain="RH (Type I)" /db_xref="Taxon:811" /clone="T9ESTyzy99b11.y1" /dev_host="DH10B (GeneHog, Invitrogen, Inc.)" /lab_host="DH10B (GeneHog, Invitrogen, Inc.)" /clone_lib="TGRH Tachyzoite Norm 5 cDNA Library" /note="Vector: phluscrit SK-; Site 1: EcoRI; Site 2: XbaI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L. Wan, Cambridge University. cDNAs were synthesized from polyA+ RNAs by Oligo d(T) priming and directionally cloned into the pCRII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was made as phagemid using ExpressIt helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc.). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."	
FEATURES	source.	
RESULT 9	CB030949	
DEFINITION	T9ESTyzy46C08.y1 TGRH Tachyzoite Norm 7 cDNA Library Toxoplasma gondii cDNA clone T9ESTyzy46C08.y1 5' similar to TR:P90613 P90613 LACTATE DEHYDROGENASE ; mRNA sequence.	
LOCUS	CB030949	
DEFINITION	LACTATE DEHYDROGENASE ; mRNA sequence.	
ACCESSION	CB030949.1	
VERSION	GI:27727321	
KEYWORDS	BST.	
SOURCE	Toxoplasma gondii Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.	
REFERENCE	Tang,K., Cole,R., Rogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.	
AUTHORS	Toxoplasma EST Project Unpublished (2001)	
JOURNAL	Contact: Clifton, S.	
COMMENT	Toxoplasma EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: toxo@wuation.wustl.edu	
TITLE	Alignment Scores:	
PRED. NO.:	9.47e-70	
SCORE:	686.50	
PERCENT SIMILARITY:	77.2%	
BEST LOCAL SIMILARITY:	64.9%	
QUERY MATCH:	40.7%	
DB:	6	
ALIGNMENT LENGTH:	772	
MACCHES:	131	
CONSERVATIVE:	25	
MISMATCHES:	45	
INDELS:	1	
GAPS:	1	

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High Quality sequence stop: 436.

Location/Qualifiers

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1. 780
/organism="Toxoplasma gondii"
/mol type="mRNA"
/strain="RH (Type I)"
/db_xref="Taxon:511"
/clone="TgB1Tzdyd6c08.Y1"
/dev_stage="Tachyzoite"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_id="TgRH Tachyzoite Norm 7 cDNA Library"
/note="Vector: pBluscript SK-; Site 1: EcoRI; Site 2: XbaI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L. Wan, Cambridge University. cDNAs were synthesized from polyA RNA by oligo d (T) priming and directionally cloned into the EcoRI site to XbaI sites of the Lambda ZAPII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using EXAssist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc.). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."

```

Qy	168	IleAlaAspLysGluValSerProArgAbpValGlyMetValIleGlyValHis	187
Qy	188	GlyAspHsMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerIle	207
Db	717	GGCATGTGATGGCCGCTTGTCGGTACATTACGTGAACGGTACCGATCCAGAG	776
Qy	208	Phe	208
Db	777	TTC	779
RESULT	10		
LOCUS	CB027630	721 bp	mRNA linear EST 13-JAN-2003
DEFINITION	TgBSTRyc98c08.y1	TgRH Tachyzoite Norm 5	cDNA Library Toxoplasma
LACRT	CDNA clone	CDNA clone	similar to TR:PR06111 P90613
DENYDROGENASE	; mRN	A sequence.	
ACCESSION	CB027630		
VERSION	CB027630.1	GI:27724602	
KEYWORDS	EST.		
SOURCE	Toxoplasma gondii		
ORGANISM	Toxoplasma gondii		
	Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida;		
	Sarcocystida; Toxoplasma.		
REFERENCE	1 (bases 1 to 721)		
AUTHORS	Tang,K., Cole,R., Pogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wyllie,T., Danté,M., Marra,M., Hillier,E., Kucaba,T., Theisberg,B., Bowes,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.		
TITLE	Toxoplasma EST Project		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Clifton, S.		
	Toxoplasma EST Project		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: toxco@watson.wustl.edu		
	Contact David Sibley (toxco@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.		
	Seq primer: -40RPr from Gibco		
	High quality sequence stop: 433.		
FEATURES	Location/Qualifiers		
source	1..721		
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	/mol_type="mRNA"		
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	/clone=TgBSTRyc98c08.y1"		
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	/lab="DH10B (GeneHog, Invitrogen, Inc.)"		
	/clone_lib=TgRH Tachyzoite Norm 5 cDNA Library"		
	/note=Vector: pBluscript SK- Site 1: EcoRI; Site 2: XbaI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L.Wan, Cambridge University.		
	CDNAs were synthesized from polyA RNAs by Oligo d(T) priming and directionally cloned into the EcoRI to XbaI sites of the Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using ExAssist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc.).		
	WARNING: the library contains a small percentage of cDNAs derived from the human host cells."		
ORIGIN			

Pred. No. :	2.21e-68	Length:	721
Score:	674.50	Matches:	130
Percent Similarity:	77.2%	Conservative:	22
Best Local Similarity:	66.0%	Mismatches:	44
Query Match:	.40.0%	Indels:	1
DB:	6	Gaps:	1
US-09-390-846-2 (1-330) x CB027630 (1-721)			
Qy	9 ArgProlysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28	FEATURES	
Db	131 AACAAAGGGTGCCTCATATGTCCTCGATCATGTTGCAAGGTGTTGCTACCTGTC 190	source	
Qy	29 serLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48	Location/Qualifiers	
Db	191 GCTCTCCGTAGCTGCTGACGCGTCTAGATGTGCAAAGGTATGCCGAGGGT 250		
Qy	49 LysAlaMetAspIleSerHisAsnSerSerValValAspAspIleLeuThrAlaThrGly 68		
Db	251 AACGCTCTTGACCTGAGCTTGACTCTGACCTTCGTCGACACCAACGTTTCGCGCT 310		
Qy	69 SerAsnSerTyrGlu--CysLeuLysGlyAlaAspValValLeuIleIleAlaGlyIle 87		
Db	311 GAGTACTCTTAACAGGCCGCTAACCGTGCCGACAGCGCTTATCGTTACGCCGGCTG 370		
Qy	88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsn 107		
Db	371 ACCAGGCGCGGAAACCGGACTCCAGTGAAGCTCCATGCTCCGGTCAAC 430		
Qy	108 IleLysIleMetArgGluValGlyAlaAlaIleIleSerTyrCysProAsnAlaPheVal 127	ORIGIN	
Db	431 TCGAAGATCATTCGCGAGATCGATGGCTCAGAAGTACTGCCAACGCCRATC 490	Alignment Scores:	
Qy	128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuIleGlyLeu 147	Pred. No. :	4.07e-68
Db	491 ATGGTGGTCACTCACCCACCGCTGACTGATGTCGAAGTTATGTCGAGCCTGGCCTC 550	Score:	671.50
Qy	148 ProIleHisArgLysCysGlyMetAlaClyMetLeuAspSerSerArgPheArgArgMet 167	Percent Similarity:	76.1%
Db	551 CGGACCAACAGATCTGGTAGGGCTGCTGAGTCAGTGGCTTCCCGATACT 610	Best Local Similarity:	61.2%
Qy	168 IleAlaLeuAspIleGluValValSerProArgAspValGlnGlyMetValIleGlyValHis 187	Query Match:	39.8%
Db	611 GTGCGCCGACGCCGCTCTCTGCTCTCCTCCGGGACGTCAGTCCACACAC 670	DB:	1
Qy	188 GlyAspHisMetValProLeuSerArgTyraIleThrValAsnGlyIlePro 204	Gaps:	1
Db	671 GSGGACGTCGACATGCTCCCGCTGACATTAACCGCTAACCGCTACCCG 721		
RESULT 11			
LOCUS	CF259970	CF259970 630 bp mRNA linear EST 11-AUG-2003	
DEFINITION		NC_0073c91h09_Y2	Nc-LIV Tachyzoite cDNA Library Neospora caninum
KEYWORDS		1	(bases 1 to 630), similar to TR:PF0613_P90613 LACTATE DEHYDROGENASE ; mRNA sequence.
ORGANISM		CF259970	
REFERENCE		CF259970.1	GI:33587543
AUTHORS			Coile, R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S., Marras, M., Gibbons, M., Ritter, B., Martin, J., Wylie, T., Theisring, B., Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Ronno, I., Tsagareishvili, R., Fedele, M., Beliygorod, L., Franklin, C., Carr, L.M., Graw, A., Maguire, L., Waddkins, J., Richey, J., Waterston, R., and Wilson, R.
JOURNAL			USA-WASHU Neospora EST Project
COMMENT			Unpublished (2000)
TITLE			Contract: Sandy Clifton Ph.D. - Neospora
JOURNAL			USA-WASHU Neospora EST Project
COMMENT			191 MetValProLeuSerArgTyrAlaThrValAsnGlyLeuProLeuSerCluPhValValby 210

Db	483	ATGGTCCCGCTGGTACATCACGGTCAACGCCATTCCAGAGTTATTAG	542		DB:	6	Gaps:	0
Qy	211	LysGlyTrpIleLysGlnGluGluAlaPaspIleValGlnDtrySthrIysValAlcGly	230	US-09-390-846-2 (1-330) x CF268212 (1-536)				
Db	543	GACGTATGTCAGAGGAGCACTCAAGGAATCAGCCAAACACAAAGGTGTCGGA	602	QY	77	GlyAlaAspValValIleIleThrAlaGlyIleThrIlysProGlyLysSerAspIys	96	
Qy	231	GlyGluIleValArgLeuIleGlyGln	239	Db	5	GGTGGCATGCGCTTACGGGTCGACCAAGGTCGGCAAGCCGACTCC	64	
Db	603	GGAAATCTGCGCTCTCGCGAG	629	QY	97	GlutnSerArgMetAspLeuIleProValAlaIleIysIleMetArgGluValGlyAla	116	
RESULT 12				Db	65	GACTGCCGAAACGATCTGCCTCTCACTCGAGATCATTCGAGATGGCTGAGTCG	124	
CP268212	CF268212	586 bp mRNA linear	EST 13-AUG-2003	QY	117	AlaIleIysSerTyrCysProAsnAlaPhaValIleAsnIleThrAlaProLeuAspVal	136	
LOCUS DEFINITION	TGSTYj13h11.y1	TGMS Tachyzote cDNA Library Toxoplasma gondii		Db	125	AACATCAAAGAAACTACTGCCAGAACCTTCATCATCTGGTCAACCACCCGTCG	184	
DEFHYDROGENASE	;	mRNA sequence ;		QY	137	MetValAlaAlaIleIuengInGluSerGlyLeuProIshIleArgIleCygIlyMetAla	156	
ACCESSION	CP268212	GI:33630165		Db	185	ATGGTCATGTATGTGGAGGCCTTGCGTCCCACATGATCTGCGTATSGCC	244	
VERSION	CP268212.1			QY	157	GlyMetIleAspSerSerArgPheArgMetIleAlaAspIleuGluValSerPro	176	
KEYWORDS				Db	245	TGATGCTGACTCTGCTGTCGACTCTGCTGTCGCGATACTGTCGCCGATC	304	
SOURCE	Toxoplasma gondii			QY	177	ArgAspValGlnGlyMetValIleGlyValHisGlyAspHIeMetValProLeuSerArg	196	
ORGANISM	Toxoplasma gondii			Db	305	CGGACGCTCCAGGCCACGGTATCGGACACACCGGCACACTGATGGTCCGTCGG	364	
BACTERIA; Alveolata; Apicomplexa; Coccidia; Bimerida;				QY	197	TyrAlaThrValAsnGlyIleProlLeuSerGluPheValIleLysGlyTrpIleLysGln	216	
SARCOCYSTIDAE; Toxoplasma.				Db	365	TACATACCGTAACGCCGCTACCGATCCAGAAGTTCATCAAAGGCCGTAGTCACGGAG	424	
REFERENCE 1 (bases 1 to 586)				QY	217	GluGluIuAlaPaspIleValGlnIysIleThrIysValAlaGlyGluIleValArgLeu	236	
AUTHORS	Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Bennett, J., Franklin, C., Teagareishvili, R., Ronko, I., Kennedy, S., Maguire, L.U., Waterston, R. and Wilson, R.			Db	425	AGCAGCTCGAGGAGATCGCTGAGCACCAAGATGTCGCTGCGCATGCCAACATCC	484	
ACCESSION	CP268212	GI:33630165		QY	237	IeuGlyGlnGlySerIalAtTyrrAlaProGlyAlaSerAlaIleGlnMetAlaGluSer	256	
VERSION	CP268212.1			Db	485	CGGGCAGGGTCCGCTTAATCGGCCGCCGCTGCGCATGCCAACATCC	544	
KEYWORDS	Toxoplasma EST Project			QY	257	TyrLeuIysPargIysArgValMetValCysSerCysTyr	270	
SOURCE	Unpublished (2001)			Db	545	TCTTGAACGAGCAAAGGGCTCATCCGTCAGCTGAC	586	
ORGANISM	Toxoplasma EST Project			RESULT 13				
COMMENT	Contact: Clifton, S.			CN621209	628 bp mRNA linear	EST 11-MAY-2004		
TOXOPLASMA EST Project	Washington University School of Medicine			LOCUS	TGSTYj13h11.y1	TGMS Tachyzote cDNA Library Toxoplasma gondii		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	Tel: 314 286 1800			DEFINITION	CDNA clone TGESTYj13h11.y1	'5' similar to TR:P90613 P90613 LACTATE DEHYDROGENASE ; mRNA sequence.		
E-mail: toxo@watson.wustl.edu				ACCESSION	CN621209	CN621209.1 GI:47130767		
Contact David Sibley (toxoeest@worcim.wustl.edu) for further information relating to organism, libraries, or clone availability.				VERSION	Toxoplasma gondii			
Seq primer: -40RP from Gibco				KEYWORDS	Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.			
High quality sequence stop: 579.				ORGANISM	1 (bases 1 to 628)			
FEATURES	Location/Qualifiers			REFERENCE	AUTHORS			
Source	/organism="Toxoplasma gondii"				Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M.,			
	/mol_type="mRNA"				Clifton, S., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M.,			
	/strain="Tachyzote"				Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,			
	/db_xref="Taxon:5811"				Ritter, E., Bennett, J., Franklin, C., Teagareishvili, R., Ronko, I.,			
	/clone="TGESTYj13h11.y1"				Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.			
	/dev_stage="Tachyzote"				TITLE Toxoplasma EST Project			
	/lab="Electroten Blue cells (Stratagene)"				JOURNAL Unpublished (2001)			
	/clone_lib="TGMS Tachyzote cDNA Library"				COMMENT Contact: Clifton, S.			
	/note="Vector: pBluescript II SK+ Site 1: EcoRI; Site 2: XbaI; The cDNA library was constructed by Keiliang Tang, and Robert Cole at Washington University. cDNA was synthesized from Poly(A)+ mRNA using an oligo-d(T) primer containing a XbaI site. Following second strand synthesis, EcoRI adaptors were ligated to the cDNA, and products were size-selected on sephacyrl S500. The cDNA were directionally cloned into the EcoRI/XbaI prepared pBluescript II SK+ vector, and electroporated into Electroten Blue cells (Stratagene). The library may contain a small percentage of host or bacterial contaminants."				Toxoplasma EST Project			
ORIGIN					Washington University School of Medicine			
Alignment Scores:					4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
Prd. No.:	1.08e-66				Tel: 314 286 1800			
Score:	659.00	Length:	586		Fax: 314 286 1810			
Percent Similarity:	71.1%	Matches:	123		Email: toxo@watson.wustl.edu			
Best Local Similarity:	63.4%	Mismatches:	27		Contact David Sibley (toxoeest@worcim.wustl.edu) for further			
Query Match:	39.0%	Indels:	44					

Fri Mar 3 09:28:00 2006

us-09-390-846-2.p2n.rst

Page 13

Db 708 GGCCTGCTGGTCCCGCTTGTCGTTACATTACCGTG 746

Search completed: March 3, 2006, 01:04:29
Job time : 3716 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 23:42:12 ; Search time 1114 Seconds
(without alignments)

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVFENTRKIAMVGSGMI.....GSIDEVEMOKAIAALDASK 330

Scoring table: BL2USM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 499997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=abss/ABSSWEB_spool/US09390846/runat_02032006_104229_4815/app_query.fasta_1
-DB=N Geneseq -Qfmt=fastaP -SUFIX=p2n_tng -MINMATCH=0 _1 -LOOPEXT=0
-UNITS=b16 -START=1 -END=1 -THR SCORE=PCT -THR MAX=100 -TRANS=human10.cdi -LIST=45
-DOCOLIGN=200 -NORM=0 -MAXLEN=500 -HEAPSIZE=500 -MINLEN=0 -MODE=LOCAL
-OUTFMT=6@o -NORM=6@t
-USER=US09390846@CCN -WAIT -DSBLOCK=100 -LONGLOG -DEB TIMEOUT=120
-NO MMAP -NEG SCORES=0 -WARN TIMEOUT=7
-WARN TIMEOUT=7 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEOP=6 -FGAPEEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELETE=7
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Database : N_Geneseq_21.*

Score Match Length DB ID Description

5 1034.5 61.3 1785 4 AAS422757 T. gondii
6 1034.5 61.3 1785 10 ADG17361 T. gondii
7 1034.5 61.3 1785 10 ADG17363 T. gondii
8 880.5 52.2 960 13 ADT13087 Bacterial
9 873.5 51.7 957 13 ADS59454 Bacterial
10 873.5 51.7 960 13 ADS6502 Bacterial
11 873.5 51.7 960 13 ADS65887 Bacterial
12 862.5 51.1 933 13 ADT45997 Bacterial
13 862.5 51.1 969 13 ADS66073 Bacterial
14 850.5 50.4 963 13 ADT43328 Bacterial
15 848.5 50.3 960 13 ADS56026 Bacterial
16 847.5 50.2 960 13 ADS56536 Bacterial
17 831.5 49.3 951 2 AAX26909 cDNA enco
18 831.5 49.3 951 2 AAX26947 P. falicip
19 740 43.8 939 13 ADT18486 Bacterial
20 709 42.0 945 13 ADT42644 Bacterial
21 706 41.8 1912 2 AAT1715 Heat resi
22 697 41.3 936 13 ADT41767 Bacterial
23 694 41.1 870 14 ACI169781 M. xanthu
C 24 694 41.1 1634 14 ACI63878 Bacterial
25 689 40.8 855 13 ADT4376 Bacterial
26 675.5 40.0 959 13 ADS61598 Bacterial
27 672 39.8 927 13 ADS57058 Bacterial
28 652.5 38.7 912 13 ADS56414 Bacterial
29 649.5 38.5 978 13 ADT43469 Bacterial
30 641 38.0 978 6 ABn93233 Staphyloc
31 641 38.0 978 13 ADS04190 Staphyloc
32 635 37.6 912 13 ADS59185 Bacterial
33 635 37.6 951 13 ADT45099 Bacterial
34 634 37.6 975 13 ADS48079 Bacterial
35 632 37.4 5024 2 AAQ55139 Staphyloc
36 632 37.4 5024 8 ABZ77355 Nucleotid
37 632 37.4 5024 10 AAL51843 Staphyloc
38 628 37.2 897 13 ADS57777 Bacterial
39 626.5 37.1 915 13 ADS58980 Bacterial
40 625.5 37.1 927 13 ADT44107 Bacterial
41 621 36.8 822 6 ABK72765 Bacterillus
42 605.5 35.9 1008 13 ADS45395 Bacterial
43 569 33.7 1005 13 ADS45382 Bacterial
44 560.5 33.2 942 13 ADT48105 Bacterial
45 518 30.7 595 13 ADS62339 Bacterial

ALIGNMENTS

RESULT 1

AAT51370 ID AAT51370 standard; cDNA to mRNA; 1679 BP.
XX AC AAT51370;
XX DT 17-OCT-2003 (revised)
XX DE Eimeria lactate dehydrogenase cDNA clone EASS2.
XX KW Lactate dehydrogenase; LDH; coccidiiosis; vaccine; vector; ds.
XX OS Eimeria acervulina; strain Houghton.

Key Location/Qualifiers
1..61 misc_RNA
/*tag= b
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280..1272
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/product= "lactate dehydrogenase"
/note= "pBluescriptII derived sequence"
1624..1679
/tag= c

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	1688		99.8	2	AAT51370	AAT51370 Eimeria 1
2	1034.5	61.3	1785	2	AAX91434	AAX91434 T. gondii
3	1034.5	61.3	1785	2	AAX91435	AAX91435 T. gondii
4	1034.5	61.3	1785	4	AAS42758	AAS42758 T. gondii

PD	16-JAN-1997.	
XX	02-JUL-1996;	96AU-00056287.
PF	03-JUL-1995;	95EP-00201801.
PR	(ALKU) AKZO NOBEL NV.	
PA	Kok JJ, Van Den Boogaart P, Vermeulen AN;	
XX	WPI: 1997-109375/11.	
DR	P-P5DB; ANW1476.	
XX	Eimeria lactate dehydrogenase protein - used for prodn. of vaccines against coccidiosis in poultry.	
PT	Claim 6; Page 20-22; 30pp; English.	
PS	A cDNA clone (AAT51370), designated EAS2, codes for the 37 kDa lactate dehydrogenase (LDH) (AAW11476) of Eimeria acervulina schizonts. It was isolated from an E. acervulina oocyst DNA library in phage lambda ZAPII by screening with antibodies raised against isolated LDH protein fraction EAS2. Nucleic acids encoding LDH, or immunologically active portions of LDH, can be used to produce LDH in host cells or organisms. The recombinant LDH, host organisms, recombinant viral vectors or naked LDH DNA can be utilised in vaccines for the protection of poultry against coccidiosis. (Updated on 17-OCT-2003 to standardise OS field)	
XX	Sequence 1679 BP; 449 A; 353 C; 408 G; 469 T; 0 U; 0 Other;	
SQ	Alignment Scores: Pred. No.: 5.99e-172 Score: 1685.00 Percent Similarity: 100.0% Best Local Similarity: 99.7% Query Match: 99.8% DB: 2	Length: 1679 Matches: 329 Conservative: 1 MisMatches: 0 Indels: 0 Gaps: 0
US-09-390-846-2 (1-330) x AAT51370 (1-1679)		
Qy	1 MetAlaValPheGluLysAsnThrArgProLysIleAlaMetGlySerGlyMetIle 20 280 ATGGGGTCCTCGAAAGATAACAGCCCCAACATTGGTGTGGGGCGCGGTGATT 339	XX
Db	21 GlyGlyThrMetAlaPheLeuCysSerLeuArgGluLeuGlyAspValValLeuPheAsp 40 340 GGAGCACCATGGCTTCCTGTGCACCTTAAGGAACCTCGAGATTTCTCTTCGAC 399	DT 24-SEP-1999 (first entry) DE T. gondii MGIS6-5 DNA sequence.
Qy	41 ValValProAlaMetPheAspSerHisAsnSerSerValVal 60 400 GTTGTAACCGAACATCGGATGGGGBAGGCCATGGTATATGCACAATTCGGTGGTT 459	XX KW Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat; T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst; Toxoplasma oocyst; 5S. OS Toxoplasma gondii.
Db	61 AspThrGlyIleThrValtryGlySerAsnSertryGluCysLeuLysGlyAlaAspVal 80 460 GACAGGGTAAACAGTATAAGCTTGATTAAGATAATGGGACCTCGGGACTTCGAC 519	XX PR 19-DEC-1997; PN WO932633-A1. PA (HESK-) HESKA CORP.
Qy	81 ValIleIleThrAlaGlyLysIleProGlyLysSerAspLysGluTrpSerArg 100 520 GTAATTAATACAGCAGGGATAACAAAAGATACTGGCTCAAAAGATGCTCTCA 579	XX PD 01-JUL-1999. XX PF 18-DEC-1998; XX PR 19-DEC-1997; PA (HESK-) HESKA CORP.
Db	101 MetAspLeuIeuproValAlaIleSerAsnLeuMetArgGluValGlyAlaAlaIleSer 120 580 ATGGATCTATTACCTGTGATTAAGATAATGGGACCTCGGGACTTCGAC 639	XX PI Milhausen MJ, Lutz SB, Ng RK; XX DR WPI: 1999-418930/35. P-PSDB; AAY29078.
Qy	121 TyrCysProAsnAlaPheValIleAsnLeuAsnProLeuAspAlaAla 140 640 TACGTGCTTATGATTGTTATATAACAAATCCATTAGTAGTGTGGTAGCTGCT 699	XX PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat infection caused by this microorganism. XX PS Example 15; Page 341-342; 381pp; English.
Db	141 LeuGlnGluSerSerGlyLeuProHisIleProGlyIleCysGlyMetAlaGlyMetLeuAsp 160 700 CCTCAAGAGTCATCAGGATACCTCATAGAAATCTGGCTATGGCTCGCATCTTGT 759	XX CC The invention provides isolated Toxoplasma gondii nucleic acids that encode immunogenic polypeptides. The T. gondii nucleic acid molecules CC

CC immunogenic proteins and antibodies to the proteins can be used to
 CC inhibit T. gondii oocyst shedding in a cat due to infection with T.
 CC gondii. They can be used for preventing T. gondii infection and for
 CC preventing the spread of T. gondii infection. They can also be used for
 CC detecting T. gondii infection. The detection method can be used to detect
 CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
 CC such as Cryptosporidium oocysts and Toxoplasma oocysts

XX Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.58e-101 Length: 1785

Score: 1034.50 Matches: 193

Percent Similarity: 77.3% Conservative: 55

Best Local Similarity: 60.1% Mismatches: 72

Query Match: 61.3% Indels: 1

DB: 2 Gaps: 1

US-09-390-846-2 (1-330) x AAX91434 (1-1785)

Qy 9 ArgProlysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28

Db 109 AGAAAGAGGGGGCCATATGGCTCGCATGATTGCTGGGCACTATGGGTACCTGTGC 168

Qy 29 SerLeuArgGluLeuGlyAspValLeuPheAspValProMetGly 48

Db 169 GCTCTGGTGCGCTCGTGAAGCTCGTCTACGATGCTGCAAAGTAGCTGCCGAGGT 228

Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68

Db 229 AAGGCTCTGACCTGACCGTGAACCAACCTTCGTCGTCGCT 288

Qy 69 SerAsnSerIleGlu---CysLeuLysGlyIleAlaAspValValIleThrAlaGlyIle 87

Db 289 GAGTACTCTAACGGCCGCTCACGGTGGGACTGGGTATCCTAACGCCGTCRG 348

Qy 88 ThrLysIleProGlyLysSerAspLysSerGluTrpSerArgMetAspLeuProValAsn 107

Db 349 ACCAAGGTGCCGGCAAGGCCGACTCGAGTGGAAACGAACTCTGTCGCCGTTCAAC 408

Qy 108 IleLysIleMetArgGluIvalGlyIleAlaAlaIleSerIleSerIleThrAlaGlyIle 127

Db 409 TCGAAGATCATTCGCGAGATCGTCGAACATCAAGAAATGACTGCCAAGACCTTCARC 468

Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaIleLeuGlnGluSerSerGlyLeu 147

Db 469 ATCGTGTCAACCAACCGCTGACTGTCTGAGTCAGGTCAAGGTCAAGGTCTGTCG 528

Qy 148 ProHsIhsArgIleLysSerAspSerSerArgLeuGlyMetArgMet 167

Db 529 CCGACCAACATGATCTGGTATGGCTGAGCTGGTGCCTGGATAC 588

Qy 168 IleAlaAspLysLeuGluIleSerProArgAspValGlyMetValIleGlyValHis 187

Db 589 GTGCGCGAAGCGCTGCTCCCGCCACGTCACCGTCACTGGCAACAC 648

Qy 188 GlyAspHisMetValProLeuSerArgIleAlaThrValAlaGlyIleProLeuSerGlu 207

Db 649 GCGGACTGTGGTCCGGTGTCCGAGTACATTACGGTAACGACTCCAGAAG 708

Qy 208 PheValLysGlyTrpIleLysGlnGluLeuIleAspAspIleValGlnLysThrIle 227

Db 709 TTCACTAAGGAGGGCTAGTCAGGAGAAGCAGTCAGGAGATGCTGAGCACCAA 768

Qy 228 ValAlaGlyGlyGluIleValArgLeuLysGlyIleLeuGly 247

Db 769 GTGTCGGCGCGAGATCGTCGCTTCGTCAGCCGCC 828

Qy 248 AlaSerAlaIleGlnMetAlaGluSerIleGlyIleGlyArgValMetValCys 267

Db 829 GCATCGGTGTCGGCATGGCACATCCTCTCTGAACTGAGTCATCCGGTC 888

Qy 268 SerCysTyrlleLeuGlnGlyIntrgylvalProCysVal 287

CC immunogenic proteins and antibodies to the proteins can be used to CC inhibit T. gondii oocyst shedding in a cat due to infection with T. CC gondii. They can be used for preventing T. gondii infection and for CC preventing the spread of T. gondii infection. They can also be used for CC detecting T. gondii infection. The detection method can be used to detect CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts CC such as Cryptosporidium oocysts and Toxoplasma oocysts	Db 889 AGTGTGFACTGCAACGGAGAGTACGGCTTGAGGACATGTTATGTTGTCCTGGCGTC 948
XX Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;	Qy 288 IleGlyGlyArgGlyIleAlaGluLeuGlyLeuGly 307
Alignment Scores:	Db 949 ATTGGAGGCGCGCATGACGCGCATGAGCTGAGTCAGCTGAGTCAGCTGAGTCAG 1008
Pred. No.: 1.58e-101 Length: 1785	Qy 308 GluLeuGlnGlySerIleAspGluValIleGlyMetGlnIysAlaIleAlaAlaLeuAsp 327
Score: 1034.50 Matches: 193	Db 1009 CAGTTCAGAGTCCCTCGAGCCGCTACAGGCGCTCATGGCGTC 1068
Percent Similarity: 77.3% Conservative: 55	Qy 328 Ala 328
Best Local Similarity: 60.1% Mismatches: 72	Db 1069 GCG 1071
Query Match: 61.3% Indels: 1	RESULT 3
DB: 2 Gaps: 1	AAX91435
DB: 1069 GCG 1071	ID AAX91435 standard; DNA; 1785 BP.
DB: 109 AGAAAGAGGGGGCCATATGGCTCGCATGATTGCTGGGCACTATGGGTACCTGTGC 168	XX XX
DB: 229 AAGGCTCTGACCTGACCGTGAACCAACCTTCGTCGTCGCT 288	24-SEP-1999 (first entry)
DB: 409 TCGAAGATCATTCGCGAGATCGTCGAACATCAAGAAATGACTGCCAAGACCTTCARC 468	DT XX
DB: 649 ATCGTGTCAACCAACCGCTGACTGTCTGAGTCAGGTCAAGGTCAAGGTCTGTCG 528	DE T. gondii MG136-5 reverse complement sequence.
DB: 709 TTCACTAAGGAGGGCTAGTCAGGAGAAGCAGTCAGGAGATGCTGAGCACCAA 768	XX XX
DB: 829 GCATCGGTGTCGGCATGGCACATCCTCTCTGAACTGAGTCATCCGGTC 888	Immunoactive protein; Toxoplasma gondii protein; oocyst shedding; cat; T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst; Toxoplasma oocyst; ss.
DB: 889 AGTGTGFACTGCAACGGAGAGTACGGCTTGAGGACATGTTATGTTGTCCTGGCGTC 948	KW KW KW KW KW OS XX
DB: 949 ATTGGAGGCGCGCATGACGCGCATGAGCTGAGTCAGCTGAGTCAGCTGAGTCAG 1008	Toxoplasma gondii.
DB: 1009 CAGTTCAGAGTCCCTCGAGCCGCTACAGGCGCTCATGGCGTC 1068	XX XX
DB: 1069 GCG 1071	PN WO932633-A1.
DB: 109 AGAAAGAGGGGGCCATATGGCTCGCATGATTGCTGGGCACTATGGGTACCTGTGC 168	PN XX
DB: 229 AAGGCTCTGACCTGACCGTGAACCAACCTTCGTCGTCGCT 288	PD 01-JUL-1999.
DB: 409 TCGAAGATCATTCGCGAGATCGTCGAACATCAAGAAATGACTGCCAAGACCTTCARC 468	XX XX
DB: 649 ATCGTGTCAACCAACCGCTGACTGTCTGAGTCAGGTCAAGGTCAAGGTCTGTCG 528	PP 18-DEC-1998;
DB: 709 TTCACTAAGGAGGGCTAGTCAGGAGAAGCAGTCAGGAGATGCTGAGCACCAA 768	PR 19-DEC-1997;
DB: 829 GCATCGGTGTCGGCATGGCACATCCTCTCTGAACTGAGTCATCCGGTC 888	XX XX
DB: 889 AGTGTGFACTGCAACGGAGAGTACGGCTTGAGGACATGTTATGTTGTCCTGGCGTC 948	(HESK-) HESKA CORP.
DB: 949 ATTGGAGGCGCGCATGACGCGCATGAGCTGAGTCAGCTGAGTCAGCTGAGTCAG 1008	XX XX
DB: 1009 CAGTTCAGAGTCCCTCGAGCCGCTACAGGCGCTCATGGCGTC 1068	PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat infection caused by this microorganism.
DB: 1069 GCG 1071	XX XX
DB: 109 AGAAAGAGGGGGCCATATGGCTCGCATGATTGCTGGGCACTATGGGTACCTGTGC 168	Example 15: Page 342-344: 381PP; English.
DB: 229 AAGGCTCTGACCTGACCGTGAACCAACCTTCGTCGTCGCT 288	CC The invention provides isolated Toxoplasma gondii nucleic acids that encode immunoactive polypeptides. The T. gondii nucleic acid molecules, immunoactive proteins and antibodies to the proteins can be used to inhibit T. gondii oocyst shedding in a cat due to infection with T. gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for detecting T. gondii infection. The detection method can be used to detect parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts such as Cryptosporidium oocysts and Toxoplasma oocysts
DB: 409 TCGAAGATCATTCGCGAGATCGTCGAACATCAAGAAATGACTGCCAAGACCTTCARC 468	XX XX
DB: 649 ATCGTGTCAACCAACCGCTGACTGTCTGAGTCAGGTCAAGGTCAAGGTCTGTCG 528	DR 1999-418930/35.
DB: 709 TTCACTAAGGAGGGCTAGTCAGGAGAAGCAGTCAGGAGATGCTGAGCACCAA 768	PT PT
DB: 829 GCATCGGTGTCGGCATGGCACATCCTCTCTGAACTGAGTCATCCGGTC 888	XX XX
DB: 889 AGTGTGFACTGCAACGGAGAGTACGGCTTGAGGACATGTTATGTTGTCCTGGCGTC 948	CC The invention provides isolated Toxoplasma gondii nucleic acids that encode immunoactive polypeptides. The T. gondii nucleic acid molecules, immunoactive proteins and antibodies to the proteins can be used to inhibit T. gondii oocyst shedding in a cat due to infection with T. gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for detecting T. gondii infection. The detection method can be used to detect parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts such as Cryptosporidium oocysts and Toxoplasma oocysts
DB: 949 ATTGGAGGCGCGCATGACGCGCATGAGCTGAGTCAGCTGAGTCAGCTGAGTCAG 1008	XX XX
DB: 1009 CAGTTCAGAGTCCCTCGAGCCGCTACAGGCGCTCATGGCGTC 1068	SQ Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;
DB: 1069 GCG 1071	Alignment Scores:
DB: 109 AGAAAGAGGGGGCCATATGGCTCGCATGATTGCTGGGCACTATGGGTACCTGTGC 168	Pred. No.: 1.58e-101 Length: 1785
DB: 229 AAGGCTCTGACCTGACCGTGAACCAACCTTCGTCGTCGCT 288	Score: 1034.50 Matches: 193
DB: 709 TTCACTAAGGAGGGCTAGTCAGGAGAAGCAGTCAGGAGATGCTGAGCACCAA 768	Percent Similarity: 77.3% Conservative: 55
DB: 829 GCATCGGTGTCGGCATGGCACATCCTCTCTGAACTGAGTCATCCGGTC 888	Best Local Similarity: 60.1% Mismatches: 72
DB: 889 AGTGTGFACTGCAACGGAGAGTACGGCTTGAGGACATGTTATGTTGTCCTGGCGTC 948	Query Match: 61.3% Indels: 1
DB: 949 ATTGGAGGCGCGCATGACGCGCATGAGCTGAGTCAGCTGAGTCAGCTGAGTCAG 1008	DB: 1-1785 Gaps: 1
DB: 1009 CAGTTCAGAGTCCCTCGAGCCGCTACAGGCGCTCATGGCGTC 1068	US-09-390-846-2 (1-330) x AAX91435 (1-1785)
DB: 1069 GCG 1071	Qy 9 ArgProlysIleAlaMetValGlySerGlyMetIleGlyGlySerGlyMetIleLeuLeuCys 28

Db	109	AGAAGGAAGGGCCATGATTGGCTCTGGATGATGGTGGCACTATGGCTACCTGTC	168		DT	17-DEC-2001	(first entry)
Qy	29	SerLeuArgGluLeuGlyAspValAlaPheAspValValProAsnMetProMetGly	48	XX	DE	T. gondii	CDNA encoding immunogenic protein PGIS65.
Db	169	GCTCTCGTGAGCTGCCCTGAGCTCGTCTACATGTTCTAACGGTCAAGGTG	228	XX	KW	Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst;	
Qy	49	IYBALamethAspIleSerHisAsnSerSerValAspThrGlyIleThrValTyrGly	68	XX	KW	Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;	
Db	229	AAGGCTCTGACTCTGCACTGCACTGAACTGGTCAACGTCAGTCAGTCGTT	288	OS	KW	oocyst shedding.	
Qy	69	SerAsnSerTyrGlu--CysLeuLysGlyAlaAspValValIleLeuThrAlaGlyIle	87	XX	XX	Toxoplasma gondii.	
Db	289	GAGTAGCTTAACGAGCCGGCTCACCGGCGACTCGCTTACGTTAACGTTACG	348	XX	XX	US2001014447-A1.	
Qy	88	ThrLysileProGlyIysSerAspAspLysGluTrpSerArgMetAspLeuLeuProValAla	107	PD	16-AUG-2001.		
Db	349	ACCAGGTGCCGGCAAGGCCGACTCGAGTGGACGCCAACGATCTGCTCCCGTTC	408	PF	18-DEC-1998;	98US-00216393.	
Qy	108	IleLeuIleMetArgGluValGlyAlaAlaIleLeuSerTyrCysProAsnAlaPheVal	127	XX	PR	19-DEC-1997;	97US-00994825.
Db	409	TGAAAGATCATTCGCAAGATGGTCAGAAACATCAGAAAGTACTGCCTACAT	468	PA	XX	(M1H/) MILHAUSEN M. J.	
Db	409	TGAAAGATCATTCGCAAGATGGTCAGAAACATCAGAAAGTACTGCCTACAT	468	PI	XX	Milhausen MJ;	
Qy	128	IleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGlusSerSerGlyLeu	147	XX	DR	WPI: 2001-529100/58.	
Db	469	ATCGCTGTCACCAAACCGCTGAGTCATGTCAGTCAGGTCATGTCAGTCATG	528	DR	P-PSDB; AAU25549.		
Qy	148	ProLysHisIargIleCysGlyMetAlaGlyMetLeuAspSerSerArgHeatArgMet	167	PT	PT	Detecting parasite oocysts or cysts in feces, comprises eluting DNA from	
Db	529	CCGACCAACATGATCTGGTATGGCTGTATGGCTGTAGTCGACTCTGAGTC	588	PT	PT	sample into aqueous solution by heating, amplifying DNA with primers	
Qy	168	IleAlaAspIleAspLysLengluValSerProArgAspValGlnGlyMetValIleGlyValHis	187	XX	PT	specific for oocysts or cysts being detected, and detecting amplification	
Db	589	GTCGCCGAACGCCGTCGTCCTCCCGCACGGTCAACGGTCAACACAC	648	XX	PT	product.	
Qy	188	GlyAspPhiMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu	207	CC	XX	Example 15; Page 165-166; 188pp; English.	
Db	649	GCGGACTGCTGATGTCGCCGTCGCCGTCATTCACCGTAACTCCAGAAG	708	CC	XX	The invention relates to detection of parasite oocysts or cysts in a	
Qy	208	PheValLysGlyTrpIleLeuGlnGluLeuValAspAspIleValGlnLysThrIle	227	CC	CC	faeces sample comprising contacting the sample with a solid support,	
Db	709	TTCATCAGGACGGCGTAGCTACGGAGAACGGATGCTAGGCAACCCAA	768	CC	CC	drying and then washing the sample with an aqueous wash solution, adding	
Qy	228	ValAlaGlyIYGluIleValArgLeuLeuGlySerAlaIleTyrAlaProGly	247	CC	CC	an aqueous elution solution and eluting DNA from the sample by heating	
Db	769	GTGTCCTGGGGAGATGTCGCTTCTCGCCAGGGTACTAGCCCCGCC	828	CC	CC	and amplifying by PCR oocyst/cyst-specific DNA and detecting the	
Qy	248	AlaSerAlaIleGlmMetAlaGluSerTyrIleLeuAspArgValMetValCys	267	CC	CC	amplification products. The method is useful for detecting parasite	
Db	829	GCATCCCTCTGCGCATGCCATGCCAACATCCTCTTCTGAAACGCCGTCATCCCGTGC	888	CC	CC	oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts	
Qy	268	SerCystYleLeuGlyIleGlyValGlnAsnHistYleLeuGlyIleGlyVal	287	CC	CC	or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia	
Db	889	AGTGTGTACTGCAACGGAGATGGCTCTGAGGACATGTCATGGCTC	948	CC	CC	cyste. The method is also useful for developing vaccines to prevent	
Qy	288	IleGlyGlyArgGlyIleLeuGlyIleLeuLeuThrAlaGlnGluArgGln	307	CC	CC	oocyte shedding in cats. The present sequence encodes an immunogenic	
Db	949	ATGGAGGGCGCACTGGGGCTCATCGAGCTGAGCTGAAACGGAGAGAG	1008	DB:	XX	protein from Toxoplasma gondii.	
Qy	308	GluLeuGlnGlySerIleAspGluValLysGluMetGlyIysAlaLeuAlaLeuAsp	327	Qy	Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;		
Db	1009	CAGTTCCAAGAACTCCGTCGACGAGTCATGGCTAACAGGGCTTGTCTTCTAG	1068	DB:	Alignment Scores:		
Qy	328	Ala 328	Qy	Pred. No. :	1.58e-101	Length:	1785
Db	1069	GCG 1071	Qy	Score:	1034.50	Matches:	193
RESLT 4			Qy	Percent Similarity:	77.3%	Conservative:	55
AB42758			Qy	Best Local Similarity:	60.1%	Mismatches:	72
ID AB42758 standard; CDNA: 1785 BP.			Qy	Query Match:	61.3%	Indels:	1
XX			DB:	DB:	4	Gaps:	1
AC AB42758;			Qy	US-09-390-846-2 (1-330) x AAS42758 (1-1785)			
XX			Qy	9 ArgProValAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys	28		
Db	109	AGAAAGAAACGTGGCATGATGGCTCTGCGATGATTGGCATACTGGCTACTGTGTC	168	Db	109	LysAlaMetAspIleSerIisAnsSerSerValValAlaSerGlyIleThrValTyGly	68
Qy	49	49 LysAlaMetAspIleSerIisAnsSerSerValValAlaSerGlyIleThrValTyGly	68	Db	229	49 LysAlaMetAspIleSerIisAnsSerSerValValAlaSerGlyIleThrValTyGly	68
Db	169	GCTCCCGTGAGCTGCCATGCCGTCAGCTTCTACATGTTGTCACCAACGTTTCGCTGCT	228	Db	229	49 LysAlaMetAspIleSerIisAnsSerSerValValAlaSerGlyIleThrValTyGly	68
Qy	69	SerAsnSerTyrGlu--CysLeuGlySerIleGlyIleLeuGlySerAspLeuLeuProValAaa	87	Qy	69 SerAsnSerTyrGlu--CysLeuGlySerIleGlyIleLeuGlySerAspLeuLeuProValAaa	87	
Db	289	GAGTACTCTAGGAGCCCGCTCACCGGTACTGCTGAACTGGTACCGCTGCTACGCGTCTGCT	348	Db	289 GAGTACTCTAGGAGCCCGCTCACCGGTACTGCTGAACTGGTACCGCTGCTACGCGTCTGCT	348	
Qy	88	ThrLysIleProGlyIleSerAspIleSerGluTrpSerArgMetAspLeuLeuProValAaa	107	Qy	88 ThrLysIleProGlyIleSerAspIleSerGluTrpSerArgMetAspLeuLeuProValAaa	107	

Qy	288	IleGlyGlyArgGlyValGluIleGluLeuGluLeuGluLeuGlnGluArgGln	307	Db	169	GCTTCGGTGGCTCGTGACTGATTTGTCAAAGGTATGCCGAGGT	228
Db	949	ATTGGAGCCGCCGCAATGAGCGCTCATGGCTCGAGCTGAACTGGAGAAG	1008	Qy	49	LysAlaLysSerHisAsnSerSerAlaValAspThrGlyIleLeuGly	68
Qy	308	GluLeuGlnGlySerIleAspGluVallysGluMetGlnLysAlaAlaLeuAsp	327	Db	229	AAAGCTCTTGACCTTGACCTGACCCATGACTCCGTGTCACCAACGTTTCCTCGTGCT	288
Db	1009	CAGTCCCAGAACGTCGTCGACGAGCTATGGGCTCAACAAACGGGTTGCTCTCAG	1068	Qy	69	SerAsnSerGlu---CysLeuLysGlyAlaAspAlaValLeuIleIleAlaGly	87
Qy	328	Ala 328		Db	289	GAGTACCTTACGAGCCGGACTCGAGTGGAGCGAAACGATCTGCCTCGTCAC	348
Db	1069	GCG 1071		Qy	88	ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAlaLeuProAlaLys	107
RESUL T	7	ADG17763	standard; DNA; 1785 BP.	Db	349	ACCAAGCTGCCGCAAGCCGACTCGAGTGGAGCGAAACGATCTGCCTCGTCAC	408
XX		ADG17763;		Qy	108	IleLysIleMetArgGluAlaAlaIleIleSerIleCysIleProAlaAlaPheVal	127
AC				Db	409	TGCGAGATCATTCATCGAGATCGTCAGAACCTCAAGAGTACTGCCAAGACCTTCATC	468
XX		26-FEB-2004 (first entry)		Qy	128	IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeu	147
DT				Db	469	ATCGTGGTCACCAACCGCTATGGCTGACTCATGTCGAAGTCATGTCAGCTGGCT	528
DE		T. gondii protein DNA #83.		Qy	148	ProHISIHSIArgIleArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMet	167
XX		Toxoplasma gondii; oocyst shedding; genetic vaccine; vaccine; ds; gene.		Db	529	CCGACCAACATGATCTGGGTATGGCTGACTCATGTCAGCTGGCTTCGCGATAC	588
OS		Toxoplasma gondii.		Qy	168	IleAlaAspIleLeuGluValSerIleArgAspValGlyMetValIleGlyValGly	187
XX		US2003194393-A1.		Db	589	GTGCGCGACGGCTGCTGCTCCTGGCACGTCAGGCCACGTCAGCCACGTCATGGCACAC	648
PD		16-OCT-2003.		Qy	188	GlyAspPhiMetValProLeuSerIleGlyValAlaValAsnGlyIleProLeuSerGlu	207
XX		PF 17-DEC-2002; 2002US-00321856.		Db	649	GCGACTGCAATGGTCCCGCTGTCCTGGTACATTACGGTGAAGCACTACCCGATC	708
PF		19-DEC-1997; 97US-0099425.		Qy	208	PheValLysIleGlyTrpIleGlyMetLeuAspIleLeuGluValSerIleArgIle	227
XX		PR 18-DEC-1998; 98US-00216393.		Db	709	TTCATCAAGGACGGCTAGTCACGGAGAAAGCTGAGGAGATCCGTGAGCACACAAA	768
PA		(MILH.) MILHAUSEN M. J.		Qy	228	ValAlaGlyGluIleLeuIleArgLeuLeuIleGlySerAlaIleIlePheProGly	247
PI		Milhausen MJ;		Db	769	GTGTCCTGGCGGAATGTCGGCTTCCTGGCACGGGTCAGCTACTAGGCCCGCC	828
DR		WPI; 2003-8999768/82.		Qy	248	AlaSerAlaIleGlnMetAlaGluSerIleIleAspArgIleBargValMetValCys	267
XX		Novel immunogenic Toxoplasma gondii proteins useful for inhibiting oocyst		Db	829	GCATGGCTGGCATGGCACATCCTTCATGGAAAGGGGTATCCCGTGC	888
PT		shedding by cats infected with Toxoplasma gondii.		Qy	268	SerCysTyrIleGluGlyGlyGlyValGlnAlaHistYleLeuGlyValProCysVal	287
PT		Example 15; SEQ ID NO 313; 198bp; English.		Db	889	AGTGTCTACTGCAACGGAGACTACGCCCTGAAGGACATGTCATGTCATGTCATGTC	948
XX		The invention relates to an isolated Toxoplasma gondii protein. The		Qy	288	IleGlyGlyArgGlyValGluIleGlySerIleGluLeuIleAlaGlnGluArgGln	307
CC		protein is useful for inhibit oocyst shedding by cats infected with		Db	949	ATTGGAGGGCGCGGATGCTGACGCGTCATCGAGCTGAACTGGGTAACAGGGAGAG	1008
CC		Toxoplasma gondii. The protein is useful for preventing or ameliorating		Qy	308	GluLeuGlnGlySerIleAspGluValIleGlySerIleAspGluValIleAlaAlaLeuAsp	327
CC		diseases caused by infection with T. gondii. The nucleic acid can be used		Db	1009	CAGTCAGAGTCATGGCTCGAGGCTCATCACAGTCATCTTCAG	1068
CC		as genetic vaccine which encodes the protein. The protein and the nucleic		Qy	328	Ala 328	
CC		acid are used as diagnostic reagents for detection of T. gondii		Db	1069	GCG 1071	
CC		infection. The present sequence is used in the exemplification of the		RESULT	8	ADT41087	
CC		invention.		ID	ADT41087	standard; CDNA; 960 BP.	
XX		Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;		XX			
DB:		Alignment Scores:		AC	ADT41087		
Pred. No.:		1.58e-101	Length:	XX			
Score:		1.034.50	Matches:	XX			
Percent Similarity:		77.3%	Conservative:	XX			
Best Local Similarity:		60.1%	Mismatches:	XX			
Query Match:		61.3%	Indels:	XX			
DB:		10	Gaps:	XX			
US-09-390-846-2 (1-330) × ADG17363 (1-1785)				DT	02-DEC-2004 (first entry)		
Qy	9	ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys	28	XX			
Db	109	AGAAAAGGAGGTGGCCATGATGGCTCGCATGATGGTACCTGGGACTATGGTGC	168	DE	Bacterial polynucleotide #17838.		
Qy	29	SerLeuArgGluLeuGlyAspValValLeuIlePheAspValValProAsnMetProMetGly	48	XX			

KW Recombinant DNA construct; transformed plant; improved plant; property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial poly nucleotide; gene; ss.
 XX OS Bacteria.

XX US2003233675-A1.

XX PD 18-DEC-2003.

XX PP 20-FEB-2003; 2003US-00369493.

XX PR 21-FBB-2002; 2002US-0360039P.

PA (CAO /) CAO Y.
 PA (HINK /) HINKLE G. J.
 PA (SLAT /) SLATER S. C.
 PA (CHEN /) CHEN X.
 PA (GOLD /) GOLDMAN B. S.

PI Cao, Y., Hinkle GJ., Slater SC., Chen X., Goldman BS;

XX DR; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX PS Claim 1; SEQ ID NO 41525; 122bp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production, or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 960 BP; 170 A; 325 C; 311 G; 154 T; 0 U; 0 Other;

SQ

KW	7 CGCAGAACATCGGGCTGATGGTCCGCATGATGGTCCGCACCTCGGCCACTCGCT 66
KW	29 SerIleArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
KW	67 GCAATCAAGAACTGGGATATGTCCTGTTCACATGCGCAAGGGAGCCGAAGGG 126
KW	49 LysAlaMetAspSerHisab1SerServAlaValAspThrGlyIleThrValtryGly 68
KW	127 ARGGCCCTGCACTGCAAGTGCGAACCTGAAAGGTTCTGATGCCAACCTCAAGGGC 186
OS	69 SerLysSerGlyCysLeuLysGlyAlaAspValValIleLeuGlyIleLeuThr 88
OS	187 GCGACAGTAGCTAGGAGCATTTGCGGCGGACGCTGATCGAACCCGGTTCCTCCG 246
OS	89 LysIleProGlyLysSerAspLysPheGluTrpSerArgMetAspLeuLeuProValAsnIle 108
OS	247 CGCARGCCGGGC-----ATGAGGCCGAGATCTCAAGACCAACCTG 291
PA	109 LysIleMetArgGluIvalGlyAlaAlaIleLysSerItyrcysProAsnAlaPheValIle 128
PA	292 GGCGCATGAGGGCTGGCGAGCGCCTGGCGCATGCCGCGACGGGTTCTGATC 351
PA	129 AsnIleThrAsnProLeuAspValMetAlaAlaLeuLysGluSerGlyLeuPro 148
PA	352 TGCATCACCAACCCCTCGAGCGMTGGTGGGGCTGGCGAATTGGGGCTGCG 411
PA	149 HisIleArgGlyCysGlyMetAlaGlyMetAlaGlySerSerArgPheArgArgMetIle 168
PA	412 CACCGAAGGTGTCGATGGCGATGCGGCGCTCTGCATCTGCCTCACTTCC 471
PA	169 AlaAspLysBlaGluValSerProArgAspValGlyMetValIleGlyValHisGly 188
PA	472 GCGGGAAATTCAAAAGTCGCGGAGGTACCGCCCTTCGCTGCGCTGGCGAACGGC 531
PA	189 AspHisMetValProLeuSerArgItyrAlaIthyValGlyLeuLeuPheIle 208
PA	532 GACACCATGGTCCCGTGATCGAGTATTCCACCGTGGCGCATCCGGCACCTG 591
PA	209 ValIleLysGlyItylIleGlyInluGluValIlePheValGlnIleThrIval 228
PA	592 ATCAGATGGCTGTTCACCCAGGGAGCTGCGCATTCGCGCATTCGCGCTCG 651
PA	229 AlaGlyGlyGlyIleLeuValArgLeuIeuGlyGlyIleSerAlaItyrTyraIaProGlyAla 248
PA	652 GCGGGGGCGAGATGTCGGCTGTCAAGACCGCTGCCTATTATGGCCGCCACC 711
PA	249 SerAlaIleGlnMetAlaGluSerItyrLeuIysAppArglySarIgylMetValIcySser 268
PA	712 AGCGGCATTCGGATGGCGATGCCGGAGCTGAGCTGCGCTGCGCTTCGTCATC 771
PA	269 CysTyrlLeuGlnGlyGlnItyrGlyValGlyIleGluLeuIleProCysValIle 288
PA	772 GCGACCTTCACGGCGCTGGCGATGCGGCTGAGCTGCGCTGCGCTTCGTCATC 831
PA	289 GlyGlyArgGlyIleGluIleGluLeuIleLeuIleGluArgGlnGluArgGlnGlu 308
PA	832 GCGAAGGACGGCGCTGGCGATGCGGCTGAGCTGCGCTGAGCTGCGCTTCGTCATC 891
PA	309 LeuGlyIleSerIleAspGluValIysGluMetGlnLysAlaIleAlaIleLeuIleAla 328
PA	892 TTGACGGTCTGGTCAAGGAACGGCAGTCAGTCAGGAACTGGTGGCAAGTCAGGCC 951
PA	329 Ser 329
Db	952 TCG 954
Db	RESULT 9
Db	ID ADS59454 standard; cDNA: 957 BP.
Db	XX XX
Db	AC AC
Db	DT DT 02-DEC-2004 (first entry)

US-09-390-846-2 (1-330) x ADT43087 (1-960)

9 ArgProIysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28

Oy

DE	Bacterial polynucleotide #14489.	9 ArgProlysiteAlaMetvalGlySerGlyMetIleGlyGlyGlyThrMetAlaPheLeuCys 28
XX	Recombinant DNA construct; transformed plant; improved plant property;	7 CGCAAAARRAATTCGCTTATTGTTTCGGCATATCGCCATTCGGCATTCGCC 66
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;	
KW	pathogen tolerance; pest tolerance; plant disease resistance;	
KW	cell cycle pathway modification; plant growth regulator;	
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;	
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;	
KW	bacterial polynucleotide; gene; ss.	
XX		
Bacteria.		
PN	US2003233675-A1.	
XX		
PD	18-DEC-2003.	
XX		
PF	20-FEB-2003; 2003US-00369493.	
XX		
PR	21-FEB-2002; 2002US-0360039P.	
XX		
PA	(CAO/) CAO Y.	
PA	(HINR/) HINKLE G. J.	
PA	(SLAT/) SLATER S. C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B. S.	
XX		
PI	Cao Y., Hinkle G.J., Slater SC., Chen X., Goldman BS;	
XX		
DR	WPI: 2004-061375/06.	
XX		
PT	New recombinant DNA construct comprising a promoter positioned to provide	
PT	expression of a polypeptide encoding a polypeptide from a	
PT	microbial source, useful for producing plants with improved properties.	
XX		
Claim 1; SEQ ID NO 38176; 122pp; English.		
DB		
CC	The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polypeptide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus and/or uptake, by modification of Photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.	
XX		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167
Percent Similarity:	72.3%	Conservative: 60
Best Local Similarity:	53.2%	Mismatches: 82
Query Match:	51.7%	Indels: 5
DB:	13	Gaps: 1
XX		
US-09-390-846-2 (1-330) x ADS62502 (1-960)		
Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;		
DB		
Alignment Scores:		
Pred. No.:	1.75e-84	Length: 960
Score:	873.50	Matches: 167

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; Plant disease resistance; cell cycle pathway modification; Plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.

Bacteria.

· US200333675-A1.

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0366039P.

(CAOY/) CAO Y.
(HINKL/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties

Claim 1; SEQ ID NO 38561; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with Plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;
 Alignment Scores:
 ed. No.: 1.75e-84 Length: 960
 score: 873.50 Matches: 167
 Percent Similarity: 72.3% Conservative: 60
 st Local Similarity: 53.2% Mismatches: 82
 Every Match: 51.7% Indexes: 5
 Canes:

-09-390-846-2 (1-330) x ADS62887 (1-960)
9 AroprotvateAlametValgusSergiyMertleguvGlyvMaraLaphtanCve 28
13 Sept. 1

SEARCHED 060 INDEXED 17A SERIALIZED 220 FILED 17C A-175-A-Orbox
NOT LOCATED PART OR LIES PRELIMINARY SPECIFICATION WHICH WAS OBTAINED
FROM USPTO AT [SEQDATA.USPTO.GOV/SEQUENCE.HTML](http://seqdata.uspto.gov/sequence.html).

Document Similarity: NO.: 3-11e-83 Length: 969 Matches: 174 Conservative: 56

Local Similarity: 53.5% Mismatches: 87
 Global Match: 13 Indels: 8 Gaps: 2

9-390-846-2 (1-330) x ADS60073 (1-969)

```

9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyYThrMetAla
   ||||| | | | | | | | | | | | | | | | | | | | | | | | |
  7 CGGAAACAAAGATAAGCCGTTATCGGATTCGGGCATGGATCGGCCG

```

Qy	29	SerLeuArgGluLeuGlyAspValValLeuPheAspValValLeuPheAspAsnMetProAsnMetProMetGly	148
Db	67	GGCCCAAGCACCTCGACGTCGTGTCGATTCGCAAGTCGAGTCGTCGATTCGCAAGTCGAGTCGTCGAGGC	126
Qy	49	LysIAlaMetAspIleSerHtBAsnSerSerValValAspIleGlyIleIleThrValTyrgly	68
Db	127	AAGGCCCTCGATATCGCGCATCGCGCATCGTGCGCCGTCGATGTTTCGATTCGCCGCTGACGGC	186
Qy	69	SerAsnertyrglycylLeuGlyIalaaspValValIleIleThrAlaIaglyIleIehr	88
Db	187	GTCAGGACTATGCCCGCATCGAGCTGCCAACGCTGATCAGCCGCTGCCGCCCCG	246
Qy	89	LysIleProGlyLysSerAspIleGlyIleSerArgMetAspLeuLeuProValAlaAlaIle	108
Db	247	CGAACGCCCTGC-----ATGAGCCGACGATCTGGGATCAACCTC	291
Qy	109	LysIleMetGluValGlyAlaAlaIleIleSerItyCysProAsnAlaPheValIle	128
Db	292	AAGGTCATGGAAACGCTGGGCCGCTCTGAGAACTATGGCCCAAAGGCCCTTCGGTCATC	351
Qy	129	AsnIleThrAsnProIleAspValMetValAlaAlaIleLeuGlnGluIeSerGlyLeuPro	148
Db	352	TGCATGCCATTCCGCTCGAGCCATGGTGCAGGCTACGGCTGCAAGTTTCCGGCTGCC	411
Qy	149	HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMetIle	168
Db	412	AAGACCCTTCAGTCGTCATGCCGCCGCTGTCGAGCTCAGGCCCTCCGCTTCCTG	471
Qy	169	AlaAspIleLeuGluValAspSerProIleGlyAspValGlyMetValIleGlyValHisGly	188
Db	472	GCGGGAAATCAAGCTCTGGTCGAGCTCAGGCCCTGAGGAGCTCACGGCTTCGTCAGCAGC	531
Qy	189	AspHisMetValProIleSerArgTyralaIleGlyIleSerGlyLeuProLeuSerGluPhe	208
Db	532	GATTCGATGGCCGATGATCGCTGCGATCCGATCGGGATCGGCATCCGCTGCCGACCTC	591
Qy	209	VallySlysGlyTrpIleGlyGluValAspAspIleValGlnLyserThrIlyVal	228
Db	592	GTCAGATGCGCTGAGCTCGAGGAGAAAGGAGAAGCTGACAGTCGTCAGCAGCCGATG	651
Qy	229	AlaGlyGlyGluIleValArgLeuIleGlyGlnGlySerAlaTyrAlaProGlyAla	248
Db	652	GCGGCCGCCGAGATCTGGCTTCAGCTGAGCTTGCTTAATAGCCGGCC	711
Qy	249	SerAlaIleGlnMetAlaGluSerItyrLeuIysArgValMetValCysser	268
Db	712	TGGGATTCGATGCCATGCGIATCCPACCTCAGGAAGAGCGCTGCTCCCTCGCT	771
Qy	269	CysThrLeuGlnGlyIleIrrGlyValGlnAsnHsTyrLeuGlyValProCysValIle	288
Db	772	GCCGCCACCTTCGCGCCAGATGGCTCAAGGGCACCTATGCGGCTCCCGTGGTCATC	831
Qy	289	GlyIgYArgGlyValGluIgylSerIleGluLeuIleThrAlaIaglyIArgGlyGlu	308
Db	832	GCGCCGGCGCCGCTGAGCGCATCATCGAGATCGCTCAACAGGGAAACGAAATG	891
Qy	309	LeuGlnGlySerIleAspGluValIysGluMetGlnLysAla-----IleIalaAla	325
Db	892	TTGGAGTTGGTGGTGGCGACCGTGGGGCTGACCGAGGCTGGCTCAAGATCGCCCG	951
Qy	326	LeuAspAlaserIlyS	330
Db	952	CAGCTCGCTTCGAAAG	966
RESULT	14		
ADT42328	ID	ADT42328 standard	CDNA: 963 BP.
XX	AC	ADT42328;	
XX	DT	02-DEC-2004	(first entry)

DE Bacterial polynucleotide #17079.
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; lignin; galactomannan;
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PP 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINKL) HINKLE G. J.
 PA (SLATR) SLATER S. C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B. S.
 PI Cao Y., Hinkle GJ, Slater SC, Chen X., Goldman BS,
 XX WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1: SEQ ID NO 40766; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g., improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved Galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/Sequence.html.
 XX
 Sequence 963 BP; 174 A; 333 C; 314 G; 142 T; 0 U; 0 Other;

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
 Db 7 CGCGCGAAGATTCGCCCCATATCGGGGCCATATCGGGCCACCTGTGGCCACATGC 66
 Qy 29 SerIeuArgGluLeuGlyAspPheValLeuPheAspValProAsnMetProMetGly 48
 Db 67 GCTCCGAAGAGTGGCACGTATCCTGTCACATGGCGAAAGGCCACCCGAGGG 126
 Qy 49 LysAlaMetAspIleSerHisAnsSerSerValAlaPheThrGlyIleThrValGly 68
 Db 127 AAGGCCCTCGACATGCCGAAGCTGGCGTGTTGGAAAGGAGTGGCCCTGAAGGCC 186
 Qy 69 SerIeuSerItyrGluCysIleLeuGlyAlaAspValValIleLeuThrAlaGlyIleThr 88
 Db 187 GCCAACGACTACGGCAGATCGCGGTGACCTCTGCAATCGCATGAGCACCCTGGGTGCCG 246
 Qy 89 LysIleProGlyLysSerAspIleLeuProValAspIleLeuProValAsnIleLeu 108
 Db 247 CGCAAGCCGGGC-----ATGAGCGGGAGACCTCTGGGCATCAACCTCG 291
 Qy 109 LysIleMetArgGluValGlyAlaAlaAlaIleSerItyrCysProAsnAlaPheValle 128
 Db 292 AAGGICATGAAGGCCGTCGGAGGGCATAGGCATCAAGGCTCAAGGCTTCCTGCATC 351
 Qy 129 AsnIleIeuAsnProLeuAspIleLeuAspSerIleLeuAspSerGlyLeuPro 148
 Db 352 TGCATCACAAACCCGCTGACGCTATGCCGCTGAGCTTCGGGGCTGCC 411
 Qy 149 HisIleArgIleCysGlyMetAlaGlySerIleLeuAspSerIleArgArgMetIle 168
 Db 412 AAGGAAAAGTCATGGATGGCTGCTGCAGCTGGCCGCTTCGCTACTTCCTCG 471
 Qy 169 AlaAspIleLeuGluValSerProArgAspValGlyIleValIleGlyValHisGly 188
 Db 472 GCTGAAGCCACCGCGCTGGAGACATCACGGCTGGACCCCTGGCCACCGGC 531
 Qy 189 AspHisMetValProLeuSerArgTyralThrValAsnGlyIleProLeuSerGluPhe 208
 Db 532 GACCCATGCTGGCGATGCTGCTGCACGCTGCGCTGCGCTGCGGAACTG 591
 Qy 209 ValIleSlyGlyIleLeuIleGlyGluIleValAspAspIleValGlnIleSerIleVal 228
 Db 592 GTCAAGCCAAGGCTGGCTGTCGAGGACAAGCTGAGGGCAGCATCGTGAAGGCCACCGCAG 651
 Qy 229 AlaGlyGlyGluLeuValArgLeuIleGlyGlyIleSerItyrAlaProGlyAla 248
 Db 652 GGCGCGGCGAGATGTCGCCCTCTGAGACCCGCTGCCCTTAACCCCGCGAG 711
 Qy 249 SerAlaIleGlnMetAlaGluSerItyrLeuIleAspArgIleSerIleValMetValCysSer 268
 Db 712 AGCGGATGCCCATGGCACCTTCACCTGAAAGCAAGAGGCGCTCTGGCGGCC 771
 Qy 269 CysteIleGlyGlyIleGlyIleGlyIleLeuGlyIleLeuGlyIleLeuGlyIleLeu 288
 Db 772 ACCTTACCTGACCGGGCAAGTAGGGCTGACGACTCTATGTCGGCTGCGCTTCATC 831
 Qy 289 GlyGlyArgGlyValGlyIleValGlyIleLeuIleLeuIleLeuIleLeu 308
 Db 832 GGCGCGGCGGCGAGAGATTCGAGTTCGAAACACAGGAGGAAAGGGATGATG 891
 Qy 309 LeuGlyGlySerIleAspGluValIleLeuIleLeuIleLeuIleLeuAspAla 328
 Db 892 TTTCGCAAAGTCGGGTGAGTCGGCTGAAGGCTGATGGAAAGCCATCCACAGC 951
 Alignment Scores:
 Pred. No.: 5.41e-82 Length: 963
 Score: 850.50 Matches: 164
 Percent Similarity: 69.8% Conservative: 60
 Best Local Similarity: 50.1% Mismatches: 92
 Query Match: 50.4% Indels: 5
 DB: 13 Gaps: 1
 RESULT 15
 ADSS6026 ID ADSS6026 standard; CDNA; 960 BP.
 XX
 AC ADSS6026;
 US-09-390-846-2 (1-330) x ADT42328 (1-963)

XX 02-DBC-2004 (first entry)

XX DT

XX DE Bacterial polynucleotide #8013.

XX KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance;

XX KW cell cycle pathway modification; plant growth regulator;

XX KW homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX KW bacterial polynucleotide; gene; ss.

XX OS Bacteria.

XX XX PN US2003233675-A1.

XX XX PD 18-DEC-2003.

XX XX PF 20-FEB-2003; 2003US-003659493.

XX XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (Cao/Y.) Cao Y.
 PA (HINKLE/G.J.) HINKLE G. J.
 PA (SLATER/S.C.) SLATER S. C.
 PA (CHEN/X.) CHEN X.
 PA (GOLDMAN/B.S.) GOLDMAN B. S.

XX PI Cao Y., Hinkle GJ., Slater SC., Chen X., Goldman BS.

XX DR WPI: 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX PS Claim 1: SEQ ID NO 311700; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic

```

CC format from USPIO at seqdata.uspto.gov/Sequence.html.
XX
SQ Sequence 960 BP; 169 A; 311 C; 325 G; 155 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.86e-82 Length: 960
Score: 848.50 Matches: 163
Percent Similarity: 70.7%
Best Local Similarity: 50.8%
Query Match: 50.3%
DB: 13 Indels: 5
Gaps: 1

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Fri Mar 3 09:27:59 2006

usb-09-390-846-2.p2n.rng

Page 16

Job time : 1118 secs

Result No.	Score	Query	Match Length	DB ID	Description	SUMMARIES
1	1688	9b_ba:*	1567	AY143388	U23207 Toxoplasma U35118 Toxoplasma AR279170 Sequence AR279171 Sequence	
2	1398	9b_in:*	2	AY143388	AY650028 Toxoplasm AY97525 Toxoplasm AJ002750 Rhizobium AB112429 Babesia b DQ060151 Plasmodiu Continuation (20 o	
3	1266	9b_iv:*	1876	AY143389	AY650028 Toxoplasm AY97525 Toxoplasm AB112429 Babesia b DQ060151 Plasmodiu Continuation (20 o	

Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: March 2, 2006, 23:46:13 ; Search time 4597 Seconds
("without alignments")
4080.561 Million cell updates/sec

Title: US-09-390-846-2
Perfect score: 1688
Sequence: 1 MAVFEKNTTRPKIAMVSGMI.....GSIDEVKEMQKAIAALDASK 330

Scoring table: BLOSUM62

XgapOp 10.0	XgapExt 0.5
YgapOp 10.0	YgapExt 0.5
FgapOp 6.0	FgapExt 7.0
DelOp 6.0	Delext 7.0

Searched: 5833141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEBL=frame_p2n.model1 -DEV=xLP
-O=abs/ABSTNEB_spool/US09308046/runat_02032006_104230_4827/app_query.fasta_1
-DB=GenEmb1
-QFMT=Fastap
-SUFFIX=p2n.rge
-MINMATCH=0.1
-LOOPEXT=0
-UNITS=bits
-START=1
-END=1
-MATRIX=blosum62
-TRANS=duman0.cod
-LIST=45
-DOCALIGN=200
-THR SCORE=PCT
-NORM=EXT
-HEAPSIZE=500
-MINLEN=0
-MAXLEN=200000000
-HOST=abs03p
-USER=US0930946@CGN
-NEG SCORES=0
-WAIT=1
-DSBLOCK=100
-LONGLOG
-DEV TIMEOUT=120
-WARN TIMEOUT=30
-THREADS=1
-XGAPOP=10
-YGAPOP=10
-XGAPEXT=0.5
-DELEXT=7

Database : GenEmb1:*

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1: 9b_ba:*
2: 9b_in:*
3: 9b_nv:*
4: 9b_om:*
5: 9b_ov:*
6: 9b_dat:*
7: 9b_ph:*
8: 9b_pr:*
9: 9b_ro:*
10: 9b_sts:*
11: 9b_sy:*
12: 9b_uin:*
13: 9b_vii:*
14: 9b_htg:*
15: 9b_pl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	AY143388	1567 bp mRNA linear acervulina lactate dehydrogenase (LDH) mRNA, complete cds.
AUTHORS	Schaap,D., Arts,G., Kroeze,J., Niessen,R., Roosmalen-Vos,S.V., Spreewenberg,K., Kuiper,C.M., Beek-Verhoeven,N.V.D., Kok,J.J., Knegte,L.R.M.A. and Vermeulen,A.N.		
LOCUS	AY143388	Bimeria acervulina	
DEFINITION	AY143388	AY143388	
ACCESSION			
VERSION	AY143388.1	GI:25989636	
KEYWORDS			An Bimeria vaccine candidate appears to be lactate dehydrogenase; characterization and comparative analysis
SOURCE			
ORGANISM			
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; Bimeria.			
REFERENCE	1 (bases 1 to 1567)		
AUTHORS	Schaap,D., Arts,G., Kroeze,J., Niessen,R., Roosmalen-Vos,S.V., Spreewenberg,K., Kuiper,C.M., Beek-Verhoeven,N.V.D., Kok,J.J., Knegte,L.R.M.A. and Vermeulen,A.N.		
TITLE	Parasitology 128 (6), 603-616 (2004)		
JOURNAL	2 (bases 1 to 1567)		
AUTHORS	Schaap,D.C.		
TITLE	Characterization and cloning of lactate dehydrogenase from three Eimeria species		
JOURNAL	Unpublished		

REFERENCE 3 (bases 1 to 1567)
AUTHORS Kok,H.J., van den Boogaart,P., Vermeulen,A.N. and Schaap,D.C.
TITLE Direct Submission
JOURNAL Submitted (20-Aug-2002) Parasitology R&D, Intervet, Wim de

FEATURES	Korverstraat, Boxmeer 5830AA, The Netherlands
SOURCE	Location/Qualifiers 1_1567 organism="Eimeria acervulina" mol_type="mRNA" /db_xref="taxon:5801" 1_1567 gene CDS /gene="LDH" /codon_start=1 /product="lactate dehydrogenase" /protein_id="AAN18975_1" /db_xref="GI: 25989637" /translation="MAVEFEKNTRPKIAMVSGCMGTTMAFLCSLRLRGLDVNLFDVVPN MPNGKAMDIHSNSVVDGITYGSNSYECIGADVVITAGTICKPGKSDKEWSRM LIFEVNKKMREYGAIAISCPNAFVNINTPDVMYAALQSSGLPHRIGGMAGMLD SSEFRMRMADKEVSPDVOGNVIGVRGDHMPLSYATVNGIPULSEFVKKGWIKOB VDDIVQTKTVKAGEEVRLLGQSSAYTAAGASLIQMAESYLRDKRKNVCSCLQLQYQG ORIGIN
	Alignment Scores: Pred. No.: 1_766-133 Length: 1567 Score: 1688.00 Matches: 330. Percent Similarity: 100.0% Conservative: 0. Best Local Similarity: 100.0% Mismatches: 0. Query Match: 100.0% Indels: 0. DB: 2 US -09-390-846-2 (1-330) x AY143388 (1-1567)
Qy	1 MetAlaValPheGluLysBanthrArgProLysLeAlaMetValGlySerGlyMetIle 20 227 ATGGGGTCCTTCGAAAGATAACGCCCAAGATTGTCTGGCCCGCTATGATT 286
Db	21 GlyGlyThrMetAlaPheLeuCysSerLeuArgGluLeuGlyAspValValLeuPheAsp 40 287 GGAGGCCACATGGCTTCTGTGAGCTGAGCTGGAAACTGGAGATGTTCTTCGAC 346
Qy	41 ValValProAsnMetProMetGlyLysAlaMetAspIleSerHisasnSerValVal 60 347 GTTGTACCCAACATGCCGATGGGGCATGGCATGATATTCGCAATTCGCTGGTGT 406
Db	61 AspThrGlyValThrValValGlySerAsnSerIleGlyCysLeuIleGlyAlaAspVal 80 407 GACAGGGATAACAGTAACTACGGCTCAATTACAGACTGCTGAAGGGTGGCACTA 466
Qy	81 ValIleIleThrAlaGlyIleIleLysIleProGlyLysSerAspLysCysLeuTrpSerIg 100 467 GTAAATAATACAGCAGGGATAACAAAGATAACCGAAAAGGCATAAACTGCTPAGA 526
Db	101 MetAspLeuLeuProValAsnIleLysIleMetArgGluValGlyAlaMetLeuAsp 120 527 ATGGATCTATTACCTGTGATAATAAGATAATGGGAGCTGGCACCAATAATCT 586
Qy	121 TyrCysProAsnAlaPheValLeuAsnIleThrAsnProLeuAspValMetValAlala 140 587 TACGTCTPATGCTATTGTTATTAATAACATACCTTGTAGTGTTAGGTGAGCTCT 646
Db	141 LeuGlnGluUserSerGlyLeuProHisIleArgIleCysGlyMetAlaIcyMetLeuAsp 160 647 CTTCAAGAGTCATGGACATCCATCATCTAGAACTGGCTGAGGCTCTGCT 706
Qy	161 SerSerArgPheArgMetIleGlyValHisGlyAspHisMetValProLeuSerArgTrpAlaThrVal 180 707 AGCTCTGTTTAGCTGTGATAATAGAGTCCTCTCAGAGTGTACAG 766
Db	181 GlyMetValIleGlyValHisGlyAspHisMetValProLeuSerArgTrpAlaThrVal 200 767 GGGATGGTACAGGTGTAACGGGATCATATGGTGCCCTAATAGATAATGCAACACT 826
Qy	201 AsnGlyIleProLeuSerGluPheValLeuLysGlyTrpIleLeuGluValAsp 220
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Qy	221 AspIleValGlnLysThrLysValAlaGlyGlyGluLeuValLeuGlyGlnGly 240 887 GATATCGTTCAAGAGACCAAGGTCGCTGAGGAAGATCTGCTATTAGAACAGC 946
Db	241 SerAlaTyrrValProGlyAlaSerAlaLeuSerAlaLeuSerAlaLeuAsp 260 947 TCGCTTACTATGCTCAGGGGTTAGCTATTGAGCTATTGAGCTTAAAGAT 1006
Qy	261 AspLYsArgValMetValCysSerCysTerLeuGlyGlnGlyValGlnAspHis 280 1007 AGAAAGAGAGTGTGTTGCTCTGACTGCAAGACAATATGGTACAGATC 1066
Db	281 TyrLeuGlyValProCysValLeGlyGlyArgGlyValGlyLysIleLeuGluGlu 300 1067 TACTTAGAGTACCTTGTTGTTGAGAGCTTGTGTTGAGATTATTGAGTGA 1126
Qy	301 LeuThrAlaGlnGluArgGlnGluLeuLysGlySerIleAspGluValLysGluMetGln 320 1127 TGACCGACAGAAAGAGAGGCTCAGGATCTAGGATCTATCGATAGGTTAGGAGATGCGAG 1186
Db	321 LysAlaLeuAlaLeuAspAlaSerIys 330 1187 AAGCTTATTGCTCTTGTATGCATCCRAG 1216
Qy	321 LysAlaLeuAlaLeuAspAlaSerIys 330 Db 1187 AAGCTTATTGCTCTTGTATGCATCCRAG 1216
Db	AY143390 Locus: Bimeria maxima lactate dehydrogenase (LDH) mRNA, linear, INV 18-MAY-2004 DEFINITION Bimeria maxima lactate dehydrogenase (LDH) mRNA, complete cds. VERSION AY143390 ACCESSION AY143390 KEYWORDS Bimeria maxima ORGANISM Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; SOURCE Bimeria maxima REFERENCE 1 (bases 1 to 1411) AUTHORS Schaap,D.,Arts,G.,Kroese,J.,Niessen,R.,Roosmalen-Vos,S.V.,Spreeuwenberg,K.,Kuijer,P.,Verhoeven,N.V.D.,Kok,J.J.,Kneegel,R.M.A. and Vermeulen,A.N. TITLE An Eimeria vaccine candidate appears to be lactate dehydrogenase; characterization and comparative analysis JOURNAL Parasitology 128 (6), 603-616 (2004) REFERENCE 2 (bases 1 to 1411) AUTHORS Schap,D.C. TITLE Characterization and cloning of lactate dehydrogenase from three JOURNAL Unpublished REFERENCE 3 (bases 1 to 1411) AUTHORS Niessen,R. and Schap,D.C. TITLE Direct Submission JOURNAL Submitted (20-AUG-2002) Parasitology R&D, Intervet, Wim de Korverstraat, Boxmeer 5830AA, The Netherlands FEATURES Location/Qualifier source 1..1411 /organism="Eimeria maxima" /mol_type="mRNA" /db_xref="GI: 25989641." /translation="WAVFEEONKRPKIALYGSMGIGGTMAFLCSLRELGDVVLFDVVPN MPMGKADMICHHNSUVUDNGTIVGYSNSYECUTNADVVIATGITKIPGKDKDEWSRM LLPVNIKIMREVGGAIKKCCECAFLINPLDVMVAQEAANYPKHMTGCMAGMLD SSRLERMIADCLHYSPHDVGMVIGVGDNMPLMRYITINGIPIQEFLGHLINKKE INNIYNTKQAGGD1VRLQGQSAYAAGPTSAILMAESTVLKDQKLFLVSSCYLNGYN

ORIGIN	VNNHYLGVPCIGKQIEQILLDLNQEKKLIQGSTDBVLENQKTAALDDAGK"	Qy	301 LeuThrAlaCingGluargGlnGluLeuGlnGlySerIleAspGluVallysGluMetGln 320
Alignment Scores:		Db	901 CTTATCGAGGGAAAAGTACTACAGGATTATTGATGAGTACTAGATGAA 960
Pred. No.:	5.8e-109	Length:	1411
Score:	1398.00	Matches:	266
Percent Similarity:	89.4%	Conservative:	29
Best Local Similarity:	80.6%	Mismatches:	35
Query Match:	82.8%	Indels:	0
DB:	2	Gaps:	0
US-09-390-846-2 (1-330) x AY143390 (1-1411)		RESULT 3	
Qy	1 MetAlaValPheGluIysAsnThrArgProlylSerAlaMetValGlySerGlyMetIle 20	AY143389	AY143389 1876 bp mRNA linear INV 18-MAY-2004
Db	1 ATGGCGTTTGAGAAAATAAGGCCCTAAGATGCCCTGGCATGATT 60	LOCUS	Bimeria tenella lactate dehydrogenase (LDH) mRNA, complete cdb.
Qy	21 GlyGlyThreMetAlaPheLeuCysserLeuArgGluLeuGlyAspValValLeuPheAsp 40	DEFINITION	Bimeria tenella lactate dehydrogenase (LDH) mRNA, complete cdb.
Db	61 GGAGGCCACATGGATTCTATGCAGTCAGCTTAAGGAATTAGGATGTTGGCTTCCTTGAC 120	VERSION	AY143389.1 GI:25989638
Qy	41 ValValProIleMetIleMetGlyAspAlaMetAsnSerIleVal 60	KEYWORDS	Bimeria tenella
Db	121 GTTGTACCTTATATGCTTATGCTGATGATTATGTCTATCTGTGTA 180	ORGANISM	Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida; Bimeriidae;
Qy	61 AspThrGlyIleThrValtYrGlySerAsnSerIleGluCysLeuGlyIysIleAspVal 80	REFERENCE	1 (bases 1 to 1876) Schaaap,D., Arts,G., Kroese,J., Niessen,R., Roosmalen-Vos,S.V., Spreeuwenberg,K., Kuijper,C.M., Beek-Verhoeven,N.V.D.; Kok,J.J., Knegetel,R.M.A. and Vermeulen,A.N.
Db	181 GACACGGTTAACTGTATACGGTCAATAGCTGTAACTAGCGCATGIA 240	AUTHORS	An Bimeria vaccine candidate appears to be lactate dehydrogenase; characterization and comparative analysis
Qy	81 ValIleIleThrAlaGlyIleThrLysIleProGlyLysSerIlePheAspGluGlySerIleAsp 100	TITLE	JOURNAL Parasitology 128 (6), 603-616 (2004)
Db	241 GTAATPAATTACTGCAGGTTAACACAAATACTCCGTTAAAGTGTCAAGA 300	REFERENCE	2 (bases 1 to 1876) Schaaap,D.C.
Qy	101 MetAspLeuIleProAlaAsnIleLeuIleThrLysIleArgGluValGlyAlaAlaIleLeuIleSer 120	AUTHORS	Characterization and cloning of lactate dehydrogenase from three Bimeria species
Db	301 ATGGATTATTATACCAGTAAATTAATAATAATGGCTGAGTGGGGCAATAAGAA 360	JOURNAL	Unpublished
Qy	121 TyrCysProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAla 140	FEATURES	3 (bases 1 to 1876) Arts,G., Kroezeh,H. and Schaap,D.C.
Db	361 TATGCCCTATGATTATAATAACAATCCTTTAGATGTAATGGTTGCTGCT 420	source	Direct Submission
Qy	141 LeuGlnGluUserSerGlyLeuProHisIleArgIleCysGlyMetAlaIleMetLeuAsp 160	gene	Submitted (20-AUG-2002) Parasitology R&D, Intervet, Wim de Korverstraat, Boxmeer 5830AA, The Netherlands
Db	421 GTACAAAGCAGCAAATGTACCPAAACATPATGATCTGTGGCATGGCAGGGATCTAGAT 480	CDS	Location/Qualifiers
Qy	161 SerSerArgPheArgMetIleAlaAspIleLeuGluValIleSerProIleArgAspValIn 180	codon_start=1	1 (bases 1 to 1876) /organism="Bimeria tenella"
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Qy	601 AATGTGTTACCTTACAAGAATTATTAAAGGATTATAATAAGGAAGAAATAAT 660	ORIGIN	
Qy	222 AspIleValGlnLyseThrIleValGlyIleLeuIleArgLeuIleGlyGlnGly 240	Alignment Scores:	
Db	661 AATATATATAAGACTAACGACTAACGAGGAGATAATGCTTAAATTAGGCAAGA 720	Pred. No.:	1.27e-97
Qy	241 SerAlaTyrIlePheLeuSerGlyAlaSerAlaLeuGlnMetAlaGluSerIleIleLysAsp 260	Score:	1266.00
Db	721 AGTGCATATTGCAACAGGTACTGTGCATATAATGCCAGAAAGTTACCTTAAGGT 780	Percent Similarity:	86.9%
Qy	261 ArgLYsArgValMetValCysSerCystyleLeuGlnGlyValGlnAsnHi 280	Best Local Similarity:	71.4%
Db	781 AAAAAAAGATTATTGTTGTTCTCTGTTACCTTAATGGAACAATAATTTAAATCAT 840	Query Match:	75.0%
Qy	281 TyrLeuGlyValProIleValGlyIleLeuGluIleLeuGlu 300	DB:	2 0
Db	841 TATCTAGGTTCTCTGTTATAATGGAGAAAGGGATGAACAATCTAGATTGAT 900	Gaps:	0
Qy	21 GlyGlyIleThrMetAlaPheLeuCysSerIleLeuArgIleLeuGlyAspValValLeuPheAsp 40	US-09-390-846-2 (1-330) x AY143389 (1-1876)	
Qy	1 MetAlaValPheGluIysAsnThrArgProlylSerAlaMetValGlySerGlyMetIle 20	Db	175 ATGGCGGTTCCTGTTCCGCGCCAGATGGCTCTGGCTCCGGCATGATC 234

US-09-390-846-2 (1-330) × AR279171 (1-1785)				
Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28				
Db 109 AGAAAGAAGTGGCCATGATGGCTCTGGCATATGGCTACTGGGC 168				
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Db 169 GCTCTCCGTCAGCTGCTGAGTCGTTCTACGATGTTGCAAGGTGCCGAGGT 228				
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Qy 69 SerAsnSerItyGlu---CysLeuLysGlyAlaAspValIleIleThrAlaGlyIle 87				
Db 289 GAGTACTCTTACGAGCCGGCTCACGGGGACTGCCATTATGTTAACGCCGTC 348				
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Qy 108 IleLysIleMetArgGluValGlyAlaAlaIleIleSerItyCysProAsnAlaPheVal 127				
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Qy 188 GlyAspPhiMetValProLeuSerArgTyrAlaAlaIleAsnGlyIleProLeuSerGlu 207				
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Qy 228 ValAlaGlyGluIleValArgLeuIleGlyGlnGlySerAlaItyTyrAlaProGly 247				
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Qy 248 AlaSerAlaIleGlnMetAlaGluSerItyIleLeuAspArgLysSerGlyAlaValMetValCys 267				
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Qy 268 SerCystyIleGluGlyGlnItyIleValGlnAsnHistItyLeuGlyValProCysVal 287				
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Qy 308 GluLeuGlnGlySerIleAspGluValLysSerGluMetGlnIlysAlaIleAlaLeuAsp 327				
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RESULT 8 AY650028 LOCUS				
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LOCUS	D0060151	951 bp	DNA	linear	INV 11-JUN-2005
DEFINITION	Plasmodium vivax strain Belem L-lactate dehydrogenase (LDH) gene, complete cds.				
ACCESSION	DQ060151	GI:66967947			
VERSION					
KEYWORDS	Plasmodium vivax (malaria parasite P. vivax)				
SOURCE	Plasmodium vivax				
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium				
REFERENCE	1 (bases 1 to 951)	Turgut-Balik, D., Akbulut, E., Shoemark, D.K., Celik, V., Moreton, K.M., Sessions, R.B., Holbrook, J.J. and Brady, R.L.			
AUTHORS	Cloning, sequencing and expression of the lactate dehydrogenase gene from the human malaria parasite, Plasmodium vivax				
JOURNAL	Biotechnol. Lett. 26 (13), 1051-1055 (2004)				
PUBMED	15218378				
REFERENCE	2 (bases 1 to 951)	Turgut-Balik, D., Akbulut, E., Shoemark, D.K., Celik, V., Moreton, K.M., Sessions, R.B., and Brady, L.R.			
AUTHORS	Direct Submission				
JOURNAL	Submitted (13-MAY-2005) Biology, Firat University, Faculty of Arts and Sciences, Elazig 23169, Turkey				
FEATURES	Location/Qualifiers				
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ORIGIN					
Alignment Scores:					
Pred. No.:	2.28E-65	Length:	951		
Score:	881.00	Matches:	176		
Percent Similarity:	71.1%	Conservative:	48		
Best Local Similarity:	55.9%	Mismatches:	89		
Query Match:	52.2%	Indels:	2		
DB:		Gaps:	1		
US-09-390-846-2 (1-330) x DQ060151. (1-951)					
Qy	9 Arg Pro LySileAlaMetValGlySerGlyMetIleGlyLysThrMetAlaPheLeuCys	Length:	951	RESULT 13	
	28	Matches:	176	BX897699_1.9/c	
		Conservative:	48	WPCOMMENT	
		Mismatches:	89	Sequence split into 20 fragments	
		Indels:	2	Begin	
		Gaps:	1	End	
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	69	Matches:	176		
		Conservative:	48		
		Mismatches:	89		
		Indels:	2		
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DB:					
Qy	11 SerAsnSerGluCysLeuLysGluAspValLeuAspValSerGlySerGlyMetIleGlyLysThrMetAlaPheLeuCys	Length:	951		
	28	Matches:	176		
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		Mismatches:	89		
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DB:					
Qy	12 GTGCCAGAACCTGGGACTCTGATGTCATGCCACCGTGACTGSC	Length:	951		
	129	Matches:	176		
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		Indels:	2		
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DB:					
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		Mismatches:	89		
		Indels:	2		
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DB:					
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		Mismatches:	89		
		Indels:	2		
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DB:					
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		Mismatches:	89		
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DB:					
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	100001	Matches:	176		
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DB:					
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	200001	Matches:	176		
	300001	Conservative:	48		
	400001	Mismatches:	89		
	500000	Indels:	2		
		Gaps:	1		
DB:					
Qy	19 BX897699_03	Length:	951		
	300001	Matches:	176		
	400001	Conservative:	48		
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	600000	Indels:	2		
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DB:					
Qy	20 BX897699_04	Length:	951		
	400001	Matches:	176		
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	600000	Mismatches:	89		
	700000	Indels:	2		
		Gaps:	1		
DB:					
Qy	21 BX897699_05	Length:	951		
	500001	Matches:	176		
	600000	Conservative:	48		
	700000	Mismatches:	89		
	800000	Indels:	2		
		Gaps:	1		
DB:					
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	900000	Indels:	2		
		Gaps:	1		
DB:					
Qy	23 BX897699_07	Length:	951		
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	900000	Mismatches:	89		
	1000000	Indels:	2		
		Gaps:	1		
DB:					
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		Gaps:	1		
DB:					
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		Gaps:	1		
DB:					
Qy	26 BX897699_10	Length:	951		
	100001	Matches:	176		
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	130000	Mismatches:	89		
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		Gaps:	1		
DB:					
Qy	27 BX897699_11	Length:	951		
	110001	Matches:	176		
	120000	Conservative:	48		
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	140000	Indels:	2		
		Gaps:	1		
DB:					
Qy	28 BX897699_12	Length:	951		
	120001	Matches:	176		
	130000	Conservative:	48		
	140000	Mismatches:	89		
	150000	Indels:	2		
		Gaps:	1		
DB:					
Qy	29 BX897699_13	Length:	951		
	130001	Matches:	176		
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	160000	Indels:	2		
		Gaps:	1		
DB:					
Qy	30 BX897699_14	Length:	951		
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	150000	Conservative:	48		
	160000	Mismatches:	89		
	170000	Indels:	2		
		Gaps:	1		
DB:					
Qy	31 BX897699_15	Length:	951		
	150001	Matches:	176		
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	170000	Mismatches:	89		
	180000	Indels:	2		
		Gaps:	1		
DB:					
Qy	32 BX897699_16	Length:	951		
	160001	Matches:	176		
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	180000	Mismatches:	89		
	190000	Indels:	2		
		Gaps:	1		
DB:					
Qy	33 BX897699_17	Length:	951		
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	180000	Conservative:	48		
	190000	Mismatches:	89		
	200000	Indels:	2		
		Gaps:	1		
DB:					
Qy	34 BX897699_18	Length:	951		
	180001	Matches:	176		
	190000	Conservative:	48		
	200000	Mismatches:	89		
	210000	Indels:	2		
		Gaps:	1		
DB:					

BX897699_19	1900001	1931047	Continuation (20 of 20) of BX897699 from base 1900001 (BX897699 Bartoneilla henselae stra	Qy	306 ArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysBalaIleAlaAla	325
Alignment Scores:				Db	14540 AACCTGCCTTGAANATCAGTCAGTCAACAGCTTGAACTTGTGAACTTGTGTTGCT	14481
Pred. No. :	2.03e-63		Length: 31047	Qy		
Score:	880.50		Matches: 169	Db	326 Leu 326	
Percent Similarity:	73.2%		Conservative: 66			
Best Local Similarity:	52.6%		Mismatches: 81			
Query Match:	52.2%		Indels: 5			
Db:	1		Gaps: 1			
US-09-390-846-2 (1-330) x BX897699_19 (1-31047)						
Qy	6 LysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAla 25			Qy	306 ArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysBalaIleAlaAla	325
Db	15425 AAAATGCACTAAAGAAATAAGCTTCTTATGGTTGGPATGATTGGGGTACTTTAGA 15366			Db	14540 AACCTGCCTTGAANATCAGTCAGTCAACAGCTTGAACTTGTGAACTTGTGTTGCT	14481
Qy	26 PheLeuCysSerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMet 45			Qy	326 Leu 326	
Db	15365 CATAATTGGACTTAAGAACATTTGGTGAATGTCCTTATTGATTCAGAAGGTATA 15306			Db	14480 GTT 14478	
Qy	46 ProMetGlyLysAlaMetAspIleSerHisAsnSerValValAspPheGlyIleThr 65			RESULT 14		
Db	15305 CCRAAAGTTAAAGCTCTTCTGATATGCCGAACTCTCACCACTGTGAGCTTGTCACT 15246			AE009456 LOCUS AE009456		
Qy	66 ValTyrglySerAsnSerItyrGlyLysGlyAlaAspValValIleIleThrAla 85			DEFINITION Brucella melitensis 16M chromosome I, section 13 of 195 of the		
Db	15245 TAAACCGGGTGTAAUCCATGATGATGAAAGTGCATGTGTGTTGTGACAGGA 15186			ACCESSION AE009456		
Qy	86 GlyIleThrLysIleProGlyLysSerAspIleAspLeuLeuPro 105			VERSION AE009456		
Db	15185 GGTRGTCAGAAAACCCTGGT-----ATGAGCCCTGATGACCCRITTTGGCC 15141			KEYWORDS complete sequence		
Qy	106 ValAsnIleIleMetArgGluValGlyAlaAlaIleLysSerItyrGlyAsnAla 125			SOURCE Brucella melitensis 16M		
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Qy	126 PheValIleAsnIleThrAsnProLeuAspValMetAlaAlaLengGluSer 145			REFERENCE Brucellaceae; Brucella.		
Db	15080 TTGGTATTTGTTACAATCCCTCTGAGCAAAGGTCCTGGGTTGAAAATTTCA 15021			AUTHORS 1 (bases 1 to 1111)		
Qy	146 GlyLeuProIshisIArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArg 165			DelVecchio,V.G., Kapatral,V., Redkar,R.J., Patra,G., Mujer,C., Los,T., Ivanova,N., Anderson,I., Bhattacharya,A., Lyridis,A., Reznik,G., Jablonski,L., Larsen,N., D'Souza,M., Bernal,A., Mazur,M., Goltzman,E., Selkov,E., Elzer,P.H., Hagius,S., O'Callaghan,D., Letesson,J.-J., Haselkorn,R., Kyrides,N. and Overbeek,R.		
Db	15020 GCTCTCCACACACAAAAAGCTGCTCTGTTAAAGATCTGACTGCATTGCGATTGCG 14961			TITLE The genome sequence of the facultative intracellular pathogen		
Qy	166 ArgMetIleAlaAspIleAspLeuSerProArgGlyMetAlaGlyMetLeuAspSerSerArgPheArg 185			JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (1), 443-448 (2002)		
Db	14960 CATTCTTACAGGAAATTAAAGCTGCTCTGTTAAAGATCTGACTGCATTGCGATTGCG 14901			PUBLMED 11756588		
Qy	186 ValHisGlyAspIleMetAlaAspIleSerArgIleAspLeuSerArgIleProLeu 205			REFERENCE 2 (bases 1 to 1111)		
Db	14900 GGACAGGGTGTCTGATGGCCCTTGGCTGTTACAGTGGTGTCTCTCA 14841			AUTHORS DelVecchio,V.G., Redkar,R.J., Patra,G. and Mujer,C.		
Qy	206 SerGluPheValLysGlyTriPheLysGlnGluGluValAspAspIleValGlnIys 225			JOURNAL Direct Submission		
Db	14840 CCCGATCTGTGAAATGGCTGGCAGAAATTGTTAGTTGTGTTAAATTCACCT 14781			JOURNAL Submitted (13-NOV-2001) Department of Veterinary Science, LSU Ag Center, 111 Dairyouple Building, Baton Rouge, LA 70803, USA		
Qy	226 ThrIleValAlaGlyGluIleLeuIleArgLeuIleGlyLysIleIleThrAla 245			REFERENCE 4 (bases 1 to 1111)		
Db	14780 ACCCGTGTGATGGTGGNGCAGAAATTGTTAGTTGTGTTAAATTCACCT 14721			AUTHORS Direct Submission		
Qy	246 ProGlyAlaSerAlaIleGlnMetAlaGluSerIleLeuIleAspArgIysAspValMet 265			JOURNAL Submitted (13-NOV-2001) Institute of Molecular Biology and Medicine, University of Scranton, Scranton, PA 18510, USA		
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Db	14660 CCTGTCGCACTTATCTTCAGGCAATATGGCTTACATCTGTTGTTCCG 14601			JOURNAL Submitted (13-NOV-2001) Laboratoire d'Immunologie et de Microbiologie, Universite de Namur, 61 rue de Bruxelles, Namur 5000, Belgium		
Qy	286 CysValIleGlyGlyArgIlyValGluLysIleIleGluLeuThrAlaGlnGlu 305			REFERENCE 6 (bases 1 to 1111)		
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Qy	306 ArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysBalaIleAlaAla			JOURNAL Direct Submission		
Db	14540 AACCTGCCTTGAANATCAGTCAGTCAACAGCTTGAACTTGTGTTGCT			JOURNAL Submitted (13-NOV-2001) Faculte de Recherche en Biologie Moleculaire, INSERM U431, Avenue Kennedy, Nimes 30900, France		
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Db 247 CGCAAAGCCGGC-----ATGAGCCGCGACGATCTGTCGGCATCACCTC 291
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Db 298 FDVSVDKVELVACKSIIADAS 318

RESULT 2

US 10-369-493-11441
; Sequence 11441, Application US/10369493

; Publication No. US20030233675A1.

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FOR PRODUCTION OF MICROBIAL PROTEINS IN PLANTS

; FILE REFERENCE: 38-0 (52052) B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; SEQ ID NO 11441 LENGTH: 319

; TYPE: PRT

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-11441

Query Match Score 873.5; DB 4; Length 320;

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; ORGANISM: Agrobacterium tumefaciens US-10-369-493-14489

Query Match Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78; Mismatches 82; Indels 5; Gaps 1;

; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

Query Match Score 873.5; DB 4; Length 320;

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; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

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Query Match Score 873.5; DB 4; Length 320;

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; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

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; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

Query Match Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78; Mismatches 82; Indels 5; Gaps 1;

; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

Query Match Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78; Mismatches 82; Indels 5; Gaps 1;

; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

Query Match Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78; Mismatches 82; Indels 5; Gaps 1;

; ORGANISM: Agrobacterium tumefaciens US-10-369-14489

RESULT 5
 US-10-369-493-20748
 ; Sequence 20748, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10 (52052) B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 12060
 ; LENGTH: 322
 ; TYPE: PRT
 ; ORGANISM: *Mesorhizobium loti*
 ; US-10-369-493-12060

Query Match 51.1%; Score 862; DB 4; Length 322;
 Best Local Similarity 53.5%; Pred. No. 1.e-77; Indels 8; Gaps 2;
 Matches 174; Conservative 56; Mismatches 87;

Qy 9 RPKIAMVGGCMIGTMAFLCSLRILGVDYLFDVNPMMGKANDISHNSVVDTGITYG 68
 Db 3 RNKTLIISGMIGTLLAMIGLKDGVLFVLDIAEGFIPGKGIDIAQSPVDFDSRLTG 62

Qy 69 SNSYECIJKGADVVITITAGITIKLPGKSDKEWSRMDLPYNIKIMREVGAAIKSYCPNAFVTI 128
 Db 63 VNDYAGIEGADCVITAGVPRKEG----MSRDLLGILNKLMEQVGLKCYAPKAFTI 117

Qy 129 NITNPLDVMVAALQESSGLPFLHRCIGMGLDSRFRMIAKLEVSFRDQGMIVGTH 188
 Db 118 CITNPLDVMWALQKFSPUPKTPHVGAGVLDSSARFRYFLAEFKVSVBDDTAFVLGSHG 177

Qy 189 DHMVPLSRYATVNGIPLSSEFVKKGWIKOBEDDIVQTKVAGGEIVRLLGQGSAYYARGA 248
 Db 178 DSNVPMPIRYSTVSGIPPLDVKMGWTSKEKLDIIVRTRDGGAEIVGJLKTGSAYAYAA 237

Qy 249 SA10MAESYLYDKRKRVMVCSYLOGQGYVONHYLGVCVIGSRGVKEKIELELTQAQRE 308
 Db 238 SALAMAESYLYDKRKRVLPCAAHLSGQYGVKGTVGVPGVVIAGCVERIEIDLNSKEDRM 297

Qy 309 LQGSIDEVYKEMQKA---IAALDASK 330
 Db 298 FEESVATVQGLTEBACVKAIPOLASK 322

RESULT 7
 US-10-369-493-17079
 ; Sequence 17079, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10 (52052) B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 12079
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: *Caulobacter crescentus*
 ; US-10-369-493-17079

RESULT 6
 US-10-369-493-12060
 ; Sequence 12060, Application US/10369493
 ; Publication No. US20030233675A1

Query Match 50.4%; Score 850.5; DB 4; Length 320;
 Best Local Similarity 51.1%; Pred. No. 2.1e-01
 Matches 164; Conservative 60; Mismatches 92; Indels 5; Gaps 1;

Qy 9 RPKIAMVGGMIGGTMMAFLCSLRLGDTYLEDVNPNGKAMDISHNSSVDTGTIVYG 68
 Db 3 RAKTALIGACMIGGTLAHAAAREEGDVLFDIAEGTPQKALDIASEASAVEFKDVAIKG 62

Qy 69 SNSYECLKGADVVITAGTTKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVI 128
 Db 63 ANDAIGADVCIVTAGIPRKPG----MSRDLIGNLKVNKAVERGCKAHAPNAFVI 117

Qy 129 NITNPLDVNVAAQLESSGPFLPHRIGCMAGLDSRFRMIAKLEVSPRDVQGMVIGVHG 188
 Db 118 CITNPLDAMWALQFSGPKERKVIGMAGLDSRFAVPLAEATGVSYDHTAWTLCGHC 177

Qy 189 DHMVPPLSRVATVNGIPLSEPFVKWIKOBBDDIVQKTKVAGGBEVRLIGQGSAYYAPGA 248
 Db 178 DDMYPMVRISTVGGGLPBLVKQGWLSQLKLDALVERTKGGEBIVALKTKGSAFYAPAE 237

Qy 249 SAQMAESTYLKDRCRVMVCSYCLQGOQGYQNHVLYGVPVCJIGGRSEVEKIELELTAQFQE 308
 Db 238 SAIANATSLKDRCRVLPAATYLTQGYGINDLVGPVYIGGAAEKFIEFETNDDEKAM 297

Qy 309 LGQSIDEVEMOKAIAALDAS 329
 Db 298 FAKSVEVGLMEACKAIISS 318

Db 299 FAKSVEVGLMEACKAIISS 318

RESULT 9
 US-10-369-493-10523

Query Match 50.2%; Score 847.5.; DB 4; Length 320;
 Best Local Similarity 52.0%; Pred. No. 4.2e-01
 Matches 167; Conservative 61; Mismatches 88; Indels 5; Gaps 1;

Qy 9 RPKIAMVGGMIGGTMMAFLCSLRLGDTYLEDVNPNGKAMDISHNSSVDTGTIVYG 68
 Db 3 RKKIALIGAGNIGITLHLAAQKELGDIVLFUVBGPYQPGKALDLSOCGPVEGFDDNIIIG 62

Qy 69 SNSYECLKGADVVITAGTTKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVI 128
 Db 63 TNDYKIGAGADVITAVGARKPG----MSRDLIGNLKVNKAVERGCKAHAPNAFVI 117

Qy 129 NITNPLDVNVAAQLESSGPFLPHRIGCMAGLDSRFRMIAKLEVSPRDVQGMVIGVHG 188
 Db 118 CITNPLDAMWALREFSGLPANKVQGAGVLDSSARTSTFLAWBFGSIRDNTFVLGGHG 177

Qy 189 DMVPLSRVATVNGIPLSEPFVKWIKOEEVDIVQKTKVAGGEIRVLLGQOSAYAPGA 248
 Db 178 DMVPLVQTQYSTNGIPLPDLVKMGLSTOEKDAIVQTRSGGGEVICLKLTKGSAFYAPAA 237

RESULT 10
 US-10-369-493-10523

Query Match 50.3%; Score 848.5; DB 4; Length 320;
 Best Local Similarity 50.8%; Pred. No. 3.3e-01
 Matches 163; Conservative 64; Mismatches 89; Indels 5; Gaps 1;

Qy 9 RPKIAMVGGMIGGTMMAFLCSLRLGDTYLEDVNPNGKAMDISHNSSVDTGTIVYG 68
 Db 3 RAKTALIGACMIGGTLAHAAIKELGDVLFDIAEGTPQKALDIQSGSEGFDATMKG 62

Qy 69 SNSYECLKGADVVITAGTTKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVI 128
 Db 63 ANSFEIAGADVCIVTAGIPRKPG----MSRDLIGNLKVNKAVERGCKAHAPNAFVI 117

Qy 129 NITNPLDVNVAAQLESSGPFLPHRIGCMAGLDSRFRMIAKLEVSPRDVQGMVIGVHG 188
 Db 118 CITNPLDAMWALQFSGPKERKVIGMAGLDSRFAVPLAEATGVSYDHTAWTLCGHC 177

Qy 189 DHMVPPLSRVATVNGIPLSEPFVKWIKOEEVDIVQKTKVAGGBEVRLIGQGSAYYAPGA 248
 Db 178 DMVPLVRLRVSTVAGIPPLPDLVQMGWTTQKLDQIVTRDGGAEVGLKTKGSAFYAPAT 237

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23237
LENGTH: 312
TYPE: PPT
ORGANISM: *Bacillus subtilis*
US-10-369-493-23237

Query Match 43.8%; Score 740; DB 4; Length 312;

Best Local Similarity 45.9%; Pred. No. 2.5e-65; Mismatches 63; Indels 12; Gaps 3;

Db 66 VYGSNSYECLKGADVVITAGITKIPGKSDKEWSRMDLIPVNICKIMREVGAAIKSYCPNA 125
64 ITGTSYETKDSIVVTTAGIARKPG ----MSRDDLVTSTNAGIMKAVTKEVRHSRPA 118

Qy 126 FVINITNPFLDVMVAALQESSGLPHHRIGCMAGMILDSSRFRMIAKDLKLEVSPRDVQGMVIG 185

Db 119 YIIVLTNPADAMTYTYKESGFPQRVIGSGVLDTARFRFTVQAELNLVSEDITGFVIG 178

Qy 186 VHGDMVPLSRYATVNGIPSEFKGWIKQEEVDIVQTKVAGGEVRLLGQSAYA 245

Db 179 GHGDDMPVIRSYGGIPLKLU---LPOERDAIVTRTRGGEVTLGGPILGNGSAYA 233

RESULT 12

US-10-369-493-16518

; Sequence 16518, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; ATTORNEY OR AGENT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; SEQ ID NO 16518

; LENGTH: 312

; TYPE: PPT

; ORGANISM: *Bacillus thuringiensis*

US-10-369-493-16518

Query Match 41.3%; Score 697; DB 4; Length 312;

; Best Local Similarity 43.5%; Pred. No. 5.2e-61; Mismatches 10; Indels 12; Gaps 3;

Db 9 RPKIAMVCGSMIGGTMAFLCSRELGVYLFDV- -VPMMPMGKAMDISHNNSSVVDTG 66

Db 5 RKKVSVIGAGFTCATFFLAQELADYVLPK---ERIDAVTRTRGGEVNLNGSAYY 64

Qy 67 YGSENSECLKGADVVITAGITKIPGKSDKEWSRMDLIPVNICKIMREVGAAIKSYCPNAF 126

Db 65 IGTSDYATDSDVWITAGIARKPG ----MSRDDLVTNSKIMSLTRDIKHSRPAI 119

Db 127 VINITNPFLDVMVAALQESSGLPHHRIGCMAGMILDSSRFRMIAKDLKLEVSPRDVQGMVIG 186

Db 120 IVVLNPVDAWTMYSVKEAGFPKERVIGSGVLDTARFRFTVQAELNLVSVDITGFVIGG 179

Db 187 HGDHMPVPLSRYATVNGIPSEFKGWIKQEEVDIVQTKVAGGEVRLLGQSAYA 246

Db 180 HGDDMPVLRVSYAGGIPLKLU---ERLBEAVTRTRGGEVTLGGNQSAYA 234

Qy 247 GASAIQMASYCLKGDRKRVNCVSCLOGYGVNHYLGPVCVIGGRVGEVRLLGQSAYA 305

Db 235 AASLVMTENAILKQRRVLPATAILEGEYGSYDLYGPVILGNGGKIEELLADEK 294

Qy 307 QELOGSIDEVKEMKAI 323

Db 295 EALDRSVESVRNMVKV 311

Qy 9 RPKIAMVCGSMIGGTMAFLCSRELGVYLFDV- -VPMMPMGKAMDISHNNSSVVDTG 65

Db 5 RKKVSVIGAGFTGATTALMAQRELGDVYLVDPQMBGPTKGRALDMLESTPVQGVDN 63

RESULT 13
 US-10-369-493-19127
 Sequence 19127, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 19127
 LENGTH: 285
 TYPE: PRT
 ORGANISM: Myxococcus xanthus
 us-10-369-493-19127

Query Match 40.0%; Score 689; DB 4; Length 285;
 Best Local Similarity 47.1%; Pred. No. 2.9e-60;
 Matches 139; Conservative 58; Mismatches 85; Indels 12; Gaps 3;

Qy 9 RPKIAMVGGMIGGTMMAFLCSRLRGDVLFDV - VPMMPGMKAMDISHSSVVDGTIV 66
 Db 1 KKKGLIGCGOINNLLAVOKSLGDKDVLYDPAAEGVKGRAALDNLAAVGDYDCRV 60
 Qy 67 YGSNSYBCKGADVVITAGITPKGSDEWSRMDLPPVNKIMREVGAIKSCKPNAFVI 126
 Db 61 KGTRDWKDVAGSDVITIZGMPRKPG---MSREDLILEINLKIMTDVAGNIKOHANAP 115
 Qy 127 VINITNPLDMVAALOESSGLPHRICGMAGMLDSSRFRMTADKLEYSPRDYQGMVIG 186
 Db 116 VINTANPLDMVAFLHKAGLPHKVMAGVQDTSRPFCAEALGSIRDVEALVIGG 175
 Qy 187 HGDDMVPLSRYATNGIPISEFYKKGWIKQEEVDIVQTKVAGGETVRLGQGSAYAP 246
 Db 176 HGDDMVPLRHTGYVPTELAK---DKUDPAITTRGEPFLVLYKGSAFGP 230
 Qy 247 GASIQMAESYLKDRKRVNVCSYLCQGVQNHYLGVQDTSRPFCAEALGSIRDVEALVIGG 301
 Db 231 ARAQIAAMESFLQDRKRVTPAAALEGGYINGYFFGVPVQIAGGYVKIHTVFL 285

RESULT 14
 US-10-369-493-9045
 Sequence 9045, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 9045
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Chloroflexus aurantiacus

Query Match 39.8%; Score 672; DB 4; Length 309;
 Best Local Similarity 43.8%; Pred. No. 1.7e-58;
 Matches 141; Conservative 54; Mismatches 111; Indels 16; Gaps 3;

Qy 9 RPKIAMVGGMIGGTMMAFLCSRLRGDVLFDV - VPMMPGMKAMDISHSSVVDGTIVG 68
 Db 2 RKKISITIGAGFVGSTTHWLAKEGDIVLJDFEVGPQGAFLDLYEASPIEGFDYDVTG 61
 Qy 69 SNSYECLGKADVVITAGITPKGSDEWSRMDLPPVNKIMREVGAIKSCKPNAFVI 128
 Db 62 TNNYADTANSDDIVTTSGAPRPG---MSREDLIVKNADITRACISQAAPLSNAVII 116
 Qy 129 NTNPFLDMVAALOESSGLPHRICGMAGMLDSSRFRMTADKLEYSPRDYQGMVIGVHG 188
 Db 117 MVNPNDAMTYLAAEVGFPKERVIGQAVGVLDAARRTFIAFMAGVSVEDYAMLIGGHG 176
 Qy 189 DMVPLSRYATNGIPISEFYKKGWIKQEEVDIVQTKVAGGETVRLGQGSAYAPGA 248
 Db 177 DMVPLRFESTSGIPVSEF---APDRLAQIVBTRKGGEIVNLKGSAYAZPAA 231
 Qy 249 GASIQMAESYLKDRKRVNVCSYLCQGVQNHYLGVQDTSRPFCAEALGSIRDVEALVIGG 308
 Db 232 ATAQMVEAVLDRKRVTPAALEGGYINGYFFGVPVQIAGGYVKIHTVFLPNEEMAL 291

Query Match 39.0%; Score 689; DB 4; Length 330;
 Best Local Similarity 47.1%; Pred. No. 2.9e-60;
 Matches 139; Conservative 58; Mismatches 85; Indels 12; Gaps 3;

Qy 309 LOGSIDEVKEMOKAALADASK 330
 Db 292 LNASKAVR-----ATLDTLK 307

RESULT 15
 US-10-369-493-13585
 Sequence 13585, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianteng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 13585
 LENGTH: 319
 TYPE: PRT
 ORGANISM: Thermoplasma volcanium
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)-(319)
 OTHER INFORMATION: unsure at all Xaa locations

Query Match 39.7%; Score 669; DB 4; Length 319;
 Best Local Similarity 42.9%; Pred. No. 3.1e-58;
 Matches 137; Conservative 68; Mismatches 91; Indels 23; Gaps 5;

Qy 9 RPKIAMVGGMIGGTMMAFLCSRLRGDVLFDV - VPMMPGMKAMDI----SHNSVVD 61
 Db 3 RKKISITIGAGFVGSTTHWLAKEGDIVLJDFEVGPQGAFLDLYEASPIEGFDYDVTG 61
 Qy 62 TGITVGSNSYECLGKADVVITAGITPKGSDEWSRMDLPPVNKIMREVGAIKSY 121
 Db 62 -GFSTDSNSYKMESSDVIYTAGARKPG---MSREDLFDKNEVEIADKLEVSPRBVQG 115
 Qy 122 CPNAFVINITNPLDMVVAALQESSGLPHRICGMAGMLDSSRFRMIAKLEVSPRBVQG 181

Db 116 SPDSIIVVVSNPADIMAYALQKISGVDPQRIMGLUGGSLLDSSRPTFLAKELDVSDVNA 175
Qy 182 MVIGYHGDDMNPPLSRYATVNGIPSEFVKKGWIKEEVDDIVQXTKVAGGEIVRLGQS 241
Db 176 FVIGSHGDMDKVPFLRYSSVAGIPIEKLKP-----EKIDAIVKTRFGGEIVNLYKAGS 230
Qy 242 AYYARGASATQMAESEYLKDOKRKNVVCSTLQQ----YGVQNHYLGVPVIGGRGVKEKI 297
Db 231 AYYARGISTAMVESVIKDKKRVPICAAVITGKRAEHYGINNKPIGVPKIGERGVVEYY 290
Qy 298 ELELTQAERQELOGSIDEV 316
Db 291 DIDFLPEELBLWKKSVASY 309

Search completed: March 2, 2006, 19:45:39

Job time : 68 secs

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OM protein - protein search, using sw mode.

Run on: March 2, 2006, 19:40:23 ; Search time 28 Seconds
(without alignments)

974.392 Million cell updates/sec

Title: US-09-190-846-2
Pefect score: 1688

Sequence: 1 MAVFEKTRPKIAMVGSIGM.....GSIDEVKEMQKATAALDAASK 330

Scoring table: BIOJUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued Patents AA:
1: /cn2_6/.ptodata/1/iaa/5 COMB.pep.*
2: /cn2_6/.ptodata/1/iaa/6 COMB.pep.*
3: /cn2_6/.ptodata/1/iaa/H1COMB.pep.*
4: /cn2_6/.ptodata/1/iaa/PICTUS COMB.pep.*
5: /cn2_6/.ptodata/1/iaa/RE1 COMB.pep.*
6: /cn2_6/.ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1688	100.0	330	2	US-09-676-882-2	Sequence 2, Appli	
2	828	49.1	315	4	PCT-US94-13796-2	Sequence 2, Appli	
3	706	41.8	329	1	US-08-013B-2	Sequence 2, Appli	
4	706	41.8	329	1	US-08-838-418-2	Sequence 2, Appli	
5	694	41.1	289	2	US-08-902-540-13486	Sequence 13486, A	
6	641	38.0	325	2	US-09-134-001C-5533	Sequence 5533, Ap	
7	464	27.5	324	2	US-09-107-532A-6486	Sequence 6486, Ap	
8	426	25.2	318	2	US-08-134-000C-4417	Sequence 4417, Ap	
9	412	24.4	317	1	US-08-748-068-3	Sequence 3, Appli	
10	412	24.4	333	1	US-08-748-068-1	Sequence 1, Appli	
11	406	24.1	354	2	US-09-949-016-8002	Sequence 8002, Ap	
12	405	24.0	351	2	US-09-949-016-11252	Sequence 11252, A	
13	405	24.0	351	2	US-09-949-016-11253	Sequence 11253, A	
14	401.5	23.8	322	2	US-08-710-729-1412	Sequence 1412, Ap	
15	401.5	23.8	322	2	US-09-710-729-2384	Sequence 2384, Ap	
16	401.5	23.8	330	2	US-09-134-001C-4328	Sequence 4328, Ap	
17	398	23.6	316	2	US-09-830-230A-561	Sequence 561, App	
18	395.5	23.4	307	2	US-09-107-532A-4274	Sequence 4274, Ap	
19	391	23.2	333	1	US-08-869-506-2	Sequence 2, Appli	
20	391	23.2	333	2	US-08-869-506-2	Sequence 2, Appli	
21	390	23.1	333	1	US-08-869-506-3	Sequence 3, Appli	
22	390	23.1	333	2	US-09-128-967-3	Sequence 4, Appli	
23	389	23.0	331	2	US-08-711-681-4	Sequence 4, Appli	
24	389	23.0	331	2	US-10-274-266-4	Sequence 4, Appli	
25	388	23.0	331	2	US-09-107-433-4752	Sequence 4752, Ap	
26	388	23.0	332	2	US-09-583-110-4591	Sequence 4591, Ap	
27	377.5	22.4	327	1	US-08-748-068-2	Sequence 2, Appli	

ALIGNMENTS

RESULT 1
US-08-676-882-2
; Sequence 2, Application US/08676882
; Patent No. 610241
; GENERAL INFORMATION:
; APPLICANT: Kok, Jacobus Johannes
; APPLICANT: van den Boogaart, Paul
; APPLICANT: Vermeulen, Arnoldus Nicolaas
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 6102041el Patient Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676, 882
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; TELEFAX: (301) 977-0847
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-676-882-2
Query Match Score 100.0%; Score 1688; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 4e-177;
Matches 330; Conservative 0; Mismatches 0; Gaps 0;
Qy 1 MAVFEKTRPKIAMVGSIGMGTMAFLCSIREGFDVYPMNGKAMIDISHNSVV 60
Db 1 MAVFEKTRPKIAMVGSIGMGTMAFLCSIREGFDVYPMNGKAMIDISHNSVV 60
Qy 61 DTGITYVGNSYEVCLKGADGVVITAGTIPKGSKDREWSRDLPPNPKIRREVGAJIKS 120

Db 61 DTGITYGGNSYECLKGADVVITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAIAKS 120 Qy 249 SAIQMAESYCLDKRKVNVCSCYLQQGYGVNHYLGVPCVIGGRVIEKIELBLTAQRQE 308
 Qy 121 YCPNAFVINTNPLDVMVAALQESSGLPHHRICGMAGMLDSRFRMIAKLEVSPRDVQ 180 Db 242 ATIEMASYCLDKRKVLICSTLEGQVGHSDTFCGGTPVQLGANGVEQVIELQINSEEKAK 301
 Db 121 YCPNAFVINTNPLDVMVAALQESSGLPHHRICGMAGMLDSRFRMIAKLEVSPRDVQ 180 Qy 309 LQGSIDEVKEMQ 320
 Qy 181 GMVTCYGHDMPLSRYATVNGIPLSEFKKGWIKQEEVDIVQTKTVAAGGEVRLLGQG 240 Db 302 FDEAIAETKRMK 313
 Db 181 GMVTCYGHDMPLSRYATVNGIPLSEFKKGWIKQEEVDIVQTKTVAAGGEVRLLGQG 240
 Qy 241 SAYAPGASAIQMAESYCLDKRKVNVCSCYLOQGYGVNHYLGVPCVIGGRVIEKIBLE 300 US-08-270-013B-2
 Db 241 SAYAPGASAIQMAESYCLDKRKVNVCSCYLOQGYGVNHYLGVPCVIGGRVIEKIBLE 300 ; Sequence 2, Application US/08270013B
 Qy 301 LTAQERQELQGSIDEVKEMOKATAALDASK 330 ; Patent No. 5682294
 Db 301 LTAQERQELQGSIDEVKEMOKATAALDASK 330 ; GENERAL INFORMATION:
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 ; STREET: Two Prudential Plaza, Suite 4900
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 61601-6780
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/270,013B
 ; FILING DATE: 01-JUL-1994
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 164701/1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Green, Robert F.
 ; REGISTRATION NUMBER: 27555
 ; REFERENCE DOCKET NUMBER: 62321
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 616-5610
 ; TELEX: (25) 3533
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 329 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-270-013B-2

RESULT 2
 PCT-US94-03796-2
 ; Sequence 2, Application PC/TUSS403796
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: GENE ENCODING THE LACTATE DEHYDROGENASE
 ; TITLE OF INVENTION: ENZYME OF PLASMODIUM FALCIPARUM
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/03796
 ; FILING DATE: 06-APR-1994
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/046,160
 ; FILING DATE: 12-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deconti, Giulio A.
 ; REGISTRATION NUMBER: 31, 903
 ; REFERENCE/DOCKET NUMBER: DCI-066CPPC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEX: (617) 227-75941
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 315 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US94-03796-2

Query Match 49.1%; Score 828; DB 4; Length 315;
 Best Local Similarity 56.8%; Pred. No. 2,1e-82; Matches 144; Conservative 51; Mismatches 93; Indels 2; Gaps 1;
 Matches 134; Score 706; DB 1; Length 329;

Qy 9 RPKIAMVGGMIGGTMAFLCSLREGLDVTLPNPMGKAMDISHNSVYVDTGTV 68
 Db 4 KAKIVLGGSGMIGGYMATIVQKNLGDVTLPVKNMPHKGKALDTSTTNMAYSNCKVSG 63 Qy 127 VINITPLDVMVAAQLEQSSGLPHHRICGMAGMLDSRFRMIAKLEVSPRDVQMVIGV 186
 Qy 69 SNSYECLKGADVVITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAIAKSYCPNAFV 128 Db 65 IGTSDDVADTDIVVTAGTARKPG---MSRDDLVTTNQKIMQVTKEVVKYSNCY 119
 Db 64 SNTYDDLAGDADVITAGGITKAPGKSDKEWNDRLLPVNIKIMREVGAIAKSYCPNAFV 123 Qy 129 NITNPLDVMVAALQESSGLPHHRICGMAGMLDSRFRMIAKLEVSPRDVQMVIGV 188
 Db 124 VVTNPVDVNVQLHQHSRGPKNKGTLGQVSLRKYVQNLVCPNDAHIVGAHG 183 Qy 187 HGDHMPLSRSRATVNGIPLSEFVKKGMKQEVVDDTQVKTRVAGGEVRLLGQSAYYAP 246
 Qy 189 DHMPLSRSRATVNGIPLSEFVKKGMKQEVVDDTQVKTRVAGGEVRLLGQSAYYAP 248
 Db 184 NKMTLKRVITVGSIPLQSFINNNKLISDABEAFDRTVNTALEIVNL-HASPYVAPA 241

Qy 247 GASATOMAESYLKDRKRVMMVCSYLOGQYGVNHYLGVPCVIGGRVEKTIELBLTAQRR 306
 Db 235 AASLIVEMVAILKDRRILPAIAYLEGEYEGIYLGVPTILGGNGIERVTEELTEEKK 294

RESULT 4

US-08-838-418-2
 ; Sequence 2, Application US/08838418
 ; Patent No. 574312
 ; GENERAL INFORMATION:
 ; APPLICANT: Segabe, et al.
 ; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
 ; TITIE OF INVENTION: DEHYDROGENASE ACTIVITY
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 ; STREET: Two Prudential Plaza, Suite 4900
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60601-6780.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.2.45
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838, 418
 ; FILING DATE: 17 MAR 1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/270, 013
 ; APPLICATION NUMBER: US 08/270, 013
 ; FILING DATE: 01 JUL 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 164701/1993
 ; FILING DATE: 02 JUL 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoover, Allen E.
 ; REFERENCE/DOCKET NUMBER: 37354
 ; INFORMATION: 78339
 ; TELEPHONE: (312) 616-5600
 ; TELEFAX: (312) 616-5700
 ; TELEX: (25) 3533
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 329 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-838-418-2

Query Match 41.8%; Score 706; DB 1; Length 329;
 Best Local Similarity 45.3%; Pred. No. 6.2e-69;
 Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;

Db 235 AASLIVEMVAILKDRRILPAIAYLEGEYEGIYLGVPTILGGNGIERVTEELTEEKK 294

Qy 247 GASATOMAESYLKDRKRVMMVCSYLOGQYGVNHYLGVPCVIGGRVEKTIELBLTAQRR 306
 Db 235 AASLIVEMVAILKDRRILPAIAYLEGEYEGIYLGVPTILGGNGIERVTEELTEEKK 294

RESULT 5

US-09-902-540-13466
 ; Sequence 13466, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902, 540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIORITY APPLICATION NUMBER: 60/217, 883
 ; PRIORITY FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 13486
 ; LENGTH: 289
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-13466

Query Match 41.1%; Score 694; DB 2; Length 289;
 Best Local Similarity 47.0%; Pred. No. 1.1e-67;
 Matches 140; Conservative 59; Mismatches 87; Indels 12; Gaps 3;

Qy 6 KNTRPKIAMVGSQMGTTMAFLSRLREGDVLFDV--VPNMPMGKMDISHNSVVDTG 63
 Db 2 QNGRKKGIGGGQIGGNALLAVQSLGDDVLYDPAEGLVKGKALDINOLAAVDGYD 61

Qy 64 ITVYGSNSYECLKGADVVITAGTAKIPGKSDKEWSRMDLPNTKIMREVGAIAKSYCP 123
 Db 62 CRYVKFTTDWIKDVAQSDDVIIAGMRPKG----MSREDLLENLKIMDVAGNIQHAP 116

Qy 124 NAFVNINNTNPDDMVVAALQESSLPPHRICGMAGMQLDSSRFRMIAKLEVSPPRDQGMV 183
 Db 117 NAFVNINNPDLDMVFAHLHKIAGPKHMVAGMAGVLDTSRFCKFVAEAIGCSIRDEALV 176

Qy 184 IGHGDHNMPLRSYATUNGIPLSBFVKGWIKOBEDDIVQTKTKVAGGEIVRLLGQSY 243
 Db 177 LGGGDDDWPLVRHTVGSVPLTELIAK----DKLDAIKTRTREGGBLVGLYKTGSAY 231

Qy 244 YAPGSAIOMAESYLKDKEKRVMMVCSYLOGQYGVNHYLGVPCVIGGRVEKTIELBL 301
 Db 232 FGPNACATAMABESELQDKRVLPAALLEGQINGYFFGVPQIGAGGVEKEVHTVEL 289

RESULT 6

US-09-134-001C-5533
 ; Sequence 5533, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134, 001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIORITY APPLICATION NUMBER: US 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIORITY APPLICATION NUMBER: US 60/055, 779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 5533
 ; LENGTH: 325
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis

Qy 9 RPKIAMVGSQMGTTMAFLSRLREGDVLFDV--VPNMPMGKMDISHNSVVDTG 66
 Db 5 RKKSIVGAGFTGTATAFLLAQKELGDVVLVDLIPQLENTPKGKALDMLAESPVLFQGDANI 64

Qy 67 YGSNSYECLKGADVVITAGTAKIPGKSDKEWSRMDLLEVNKIMREVGAIAKSYCPNAF 126
 Db 65 IGTSDYADTADSIVTVGIARKPG----MSRDDLVTTNOKIMKQVTKEVVYKSPNCY 119

Qy 127 VINITNPDDMVVAALQESSLPPHRICGMAGMQLDSSRFRMIAKLEVSPPRDQGMV 186
 Db 120 IIVLTNPVDAMTYVPEKSGFPKNRIVGSGVLDTARFTFVAEELNISKDVTGFVLG 179

Qy 187 HGDHMVPLSRYATUNGIPLSBFVKGWIKOEVYDIOVTKVAGGEIVRLLGQGSAYAP 246
 Db 188 HGDDMWPLVRYSYAGGIPPEKLIPK----DRDAIVERTRGGEETVNLNGNSAYAP 234

US-09-134-001C-5533

Query Match 38 0%; Score 641; DB 2; Length 325;
Best Local Similarity 41.6%; Pred. No. 0.98-62;
Matches 132; Conservative 71; Mismatches 103; Indels 12; Gaps 4;

Qy 9 RPKIAMVGGMIGGTMMAFLCSLRBLGVDLFLD--VVPPNPMKAMDISHNSVVDGTIV 66
Db 16 RRKSTIIGGHTGDTLAFQKSLKEWRSRMLPNUKIMREGAIAKSYPNAF 126

Qy 67 YGSNSYECLRGADVITITAGITKIPGKSKDLSRQSEMAKGALDILSFGPFWGFDTSV 75
Db 76 HGSVNIEDKDSDIVMTAG--IPRKSGC-MTREELVQTNEQVRETQATYAPHIS 130

Qy 127 VINITNPFLYVVAQLESSGLPHRIGMAGLDSRFRMIAKDLKLESPRDQGMVIG 186
Db 131 IIVITNPVDMTAFKAQGFPERIIGGSGILDAARTRTFIAELNYSVQDNGFVLGG 190

Qy 187 HGDHMVPLSRYATVNGIPSEFVKKGWIKMEEEDIVOKTKVAGGEIVRLGGGSAYAP 246
Db 191 HGDHMPLJLNNTHINGIPV----KHLISSEKIDQIVRTRKGAEIVALLGGGSAYAP 245

Qy 247 GASAIQMAESYLKDCKRVMVCSCYLOGQGVQNHYLGVCVIGGRVKEELTAQR 306
Db 246 ATAYETIDAIFNDKRKLPSIASYLEGETGCSDCIFGYPTIIGYQIEKKIEVDMNNDY 305

Qy 307 QELOQSIDEVKEMOKA 323
Db 306 QQLOHSAAQAVSEVRNSL 322

RESULT 7
US-09-107-532A-6486
Sequence 6486, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02434

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
NAME: Arinieillo, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 6486:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1..324
SEQUENCE DESCRIPTION: SEQ ID NO: 6486:

US-09-107-532A-6486

Query Match 27.5%; Score 464; DB 2; Length 324;
Best Local Similarity 32.8%; Pred. No. 2.8e-12;
Matches 106; Conservative 72; Mismatches 135; Indels 10; Gaps 5;

Qy 3 VFEKNTRPKIANVGSMIGGTMMAFLCSLREL-GDVVLFDFVVPNMPMKGAMDISHNSSVVD 61
Db 9 LFKKTSRKVVIVGTVGFTGTSAYAMTNQISNELLVNOEKAEBALDLDGAWGD 68

Qy 62 TGITVGSNSYECLKGADVVITAGITKIPGKSDKEMWSRMOLLPVNTKIMREVGAAIKSY 121
Db 69 ENVAVW-SGGYBECKDADIVVITAGINQKPGQ----SRDLVKTNASIMROIVEKIMGS 122

Db 122 CPNAFVININTPLDVMVVAQLESSGLPHRIGMAGLDSRFRMIAKDLKLESPRDQVG 181
Qy 123 GFPGIIVVASNEVDILTYIAWNESSLTSRVIGTGTLDTTRFRKETALKKVDPRSVHG 182

Db 182 NYIGVHGDMMYPLSRATVNGIPLSEPEVQKTPKVAEGGEIVRLGGQG 240
Db 183 YLIGEHGSEVAASHTVVGKPVFLIVEKDHRIAQEDLVIAKRNAAYIIL--RKK 240

Qy 241 SAYAPGASAIQMAESYLKDCKRVMVCSCYLOGQGVQNHYLGVCVIGGRVKEKILE 300
Db 241 ATYYGIGMSSTARIVKATLNNEOAVLPVSAYLTGEYEDKDFITGVPSIVDENGREVYEL 300

Qy 301 LTQAERQELQGSDIDEVKEMOKA 323
Db 301 INEEEKAMFSKSTSALREVLYV 323

RESULT 8
US-09-134-000C-4417
Sequence 4417, Application US/09134000C
Patent No. 6617156

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812
SEQ ID NO: 4417
LENGTH: 318

TYPE: PRT
ORGANISM: Enterococcus faecalis

US-09-134-000C-4417

Query Match 25.2%; Score 426; DB 2; Length 318;
Best Local Similarity 30.3%; Pred. No. 4.1e-38;
Matches 99; Conservative 80; Mismatches 130; Indels 18; Gaps 7;

Qy 1 MAVPERKTRPKIANVGSMIGGTMMAFLCSLREL--DVVLFDVVPNMPMKGAMDISHNS 57
Db 2 MKVFNK---KVAIGTGTVGFTSIAY--SMINQGIANELLVIDAKSEGETIDLDGV 55

Qy 58 SVVDTGATVGSNSYECLKGADVVITAGITKIPGKSDKEMWSRMOLLPVNTKIMREVGAA 117
Db 56 SWGQENTVNWAGDYQNC-QNADIVVTTAGAQKPGQ----SRDLVSVINAEMKTVNN 109

Qy 118 IKSYCPNAFVININTPLDVMVAAQLESSGLPHRIGMAGLDSRFRMIAKDLKLESPR 177

Db 110 IMKSGPDGLVIAANPVDLTYVANQASSGLPVSTLIGTTLTDTRFKELSQRLAIDR 169
 Qy 178 DVQGMVIGHGDHMPPLSRYATVINGIPLSEFV-KKGWIKOEEVDDIVQTKVAGGEIVRL 236
 Db 170 NVHGRTIGERGDSYEAVWNSHTMIGTKPILEIVDTERLSDDLPTISDVKNTAYEIID- 228
 Qy 237 LGQQSAYAYAGASATQMAESYLKDKRVRNVCSCYLGQGVQNHYLGVCVIGERGVENI 296
 Db 229 -RKQATYYGIGMSTARIVKALNNEOAILPVSAVLGQGQQDVFTGIAVVGNGQVTDI 287
 Qy 297 IEELTAQERQELQGOSIDEDEVKEMOKAI 323
 Db 288 JELNLNAAEKELFQKSVTQLQVMASL 314

RESULT 9
 US-08-748-068-3
 Sequence 3, Application US/08748068
 General Information:
 Applicant:
 Title of Invention: Chiral Synthesis
 Number of Sequences: 15
 Computer Readable Form:
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patentin Release #1.0, Version #1.25 (BPO)
 Current Application Data:
 Application Number: US/08/748,068
 Filing Date: 12-NOV-1996
 Classification: 435
 Prior Application Data:
 Application Number: 08/256,959
 Filing Date: 05-OCT-1994
 Application Number: GB 92 02033.8
 Filing Date: 30-JAN-1992
 Prior Application Data:
 Application Number: GB 92 04702.6
 Filing Date: 04-MAR-1992
 Prior Application Data:
 Application Number: GB 93/00204
 Sequence Characteristics:
 Length: 317 amino acids
 Anti-sense: NO
 Fragment Type: internal
 Feature:
 Name/Key: Modified-site
 Location: (15^16)
 Other Information: /note= "- numbering discontinuity"
 Feature:
 Name/Key: Modified-site
 Location: (28^29)
 Other Information: /note= "- numbering discontinuity"
 Feature:
 Name/Key: Modified-site
 Location: (29^30)
 Other Information: /note= "- numbering discontinuity"
 Feature:
 Name/Key: Modified-site
 Location: (30^31)
 Other Information: /note= "- numbering discontinuity"
 Feature:
 Name/Key: Modified-site
 Location: (40^41)
 Other Information: /note= "- numbering discontinuity"

FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (69^70)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (73^74)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (83^84)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (115^116)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (138^139)
 OTHER INFORMATION: /note= "---- numbering
 OTHER INFORMATION: discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (176^177)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (181^182)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (195^197)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (211^212)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (234^235)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (230^231)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (251^252)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (264^265)
 OTHER INFORMATION: /note= "---- numbering
 OTHER INFORMATION: discontinuity"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: (286^287)
 OTHER INFORMATION: /note= "- numbering discontinuity"
 US-08-748-068-3

Query Match 24.4%; Score 412; DB 1; Length 317;
 Best Local Similarity 28.1%; Pred. No. 1.4e-36;
 Matches 89; Conservative 79; Mismatches 139; Indels 10; Gaps 5;

Qy 5 EKNTRPKIAMVGSIGMTAFLCSRELGD-VVLFDVPMMPGKAMDISHSNSVDTG 63
 Db 2 KNGGARVVGAGFVGASYVPALMNQGIADEIVLDIANESKAIGDAMDFNICKVAFKP 61
 Qy 64 ITVYGSNSYECLKGADVVIIITAGITKLPGKSDKEWSRMDLLPVNIKMRVEGAIAKSVC 123
 Db 62 VDIWHGDXDDC-RDADLVVICAGANQKPGE---TRLDLVKNAIFRSIVVESMASGP 115
 Qy 124 NAFVNINTNPFLDVMAALQESSGLPPIHRICGMAGMLDSSRFRMIADKLEYSPRDDQGMV 183

RESULT 11
US-09-949-016-8002
Sequence 8002, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 8002
LENGTH: 354
TYPE: PRT
ORGANISM: Human
US-09-949-016-8002

Query Match 24.1%; Score 406; DB 2; Length 354;
Best Local Similarity 29.3%; Pred. No. 7.8E-36;
Matches 99; Conservative 130; Indels 34; Gaps 10;

Qy 5 EKNTTRPKTAMVGGMIGGTMAFLCSLRBLGD-VVLDVVPNPMGMKAMDISHNSVVDTG 63
Db 35 DENSOCKITIVTGAVGMACAISLKLDAELALVDVALDKLGEMMDLQHGSLLFFSTS 94

Qy 64 ITYGGNSYECLKGADVVITAGTKIPGKSDKEWSRDLPLPNIKIMREVGAIKSICP 123
Db 95 KITSKGKD-YVSVASNSRIVTVTAGQRQGE-----TRIALQVNVAIMKSIPIAVHYSP 148

Qy 124 NAVVINTINPNDLYMVAALQESSGLPHERICGMAGMLDSSRFRMIAKLEVSPrDVQGMV 183
Db 149 DCKILWVSNPVDLTYIWKISGLPTRVIGSCCNLDSARFYLIGEVHTSCHWI 208

Qy 184 IGYHDHMVPLSRYATVNGIPL-----SEPVKGKTIKQEEVDDIVQTKVAGGEIVR 235
Db 209 IGEHGDSYSPVPLSGVNTAGVALKTLDPLKLTGTDSEKHW-----KNHKQVIQSAYEIK 262

Qy 236 LLGGQGAYAPGASAQNAESYKDRGRVMVCSCYLOGQGYVNH-YLGVPCTYGGREGE 294
Db 263 LKGYS-WAIGUSVMDLVGSIKLNRLRHPVSTMVKGLYGIKEELFLSIPCVLGRNGVS 320

Qy 295 KILEELTAQERQELQGSDIDEVKEMQ 321
Db 321 DVYRKINLSEEALFKKSAETLWNIQ 347

RESULT 13
US-09-949-016-11253
Sequence 11253, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 11253
LENGTH: 351
TYPE: PRT
ORGANISM: Human
US-09-949-016-11253

RESULT 12
US-09-949-016-11252
Sequence 11252, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

Query Match 24.0%; Score 405; DB 2; Length 351;
 Best Local Similarity 30.9%; Pred. No. 1e-35; Matches 101; Conservative 72; Mis matches 130; Indels 24; Gaps 7;

Qy 5 EKNTRPKTAMVGSIGCTMAFLCSLRELG-D-VVLFDVNPMPKAMDISSHNSSSVVDTG 63
 Db 35 DENSQCKTIVGTAAGVNAACATISLLQDALEALVDAFLDKKGEMMDLQNGSLFFESTS 94

Qy 64 ITIYGSNSYECKGADVVIITAGTIKIPGKSDKEWSBMDLPLWNIKIMBEVGAAIKSYCP 123
 Db 95 KITSGKD-YSVSANSRIVVTAGAROQE-----TRIALVQRNVAIMKSTIPIAIVHYS 148

Qy 124 NAVFVININPLDWNVAALQESSGLPHHRIGMAGMLSSRFRMIAKDEVSPPDVQGMV 183
 Db 149 DCKLVNVSPVUDLITYWIKISLUPVTRIGSCNLDSSARFYLIGEKGH/PPTSCHGW 208

Qy 184 IGVGDHNWVPLSLRYATVNGIPL-----SEFVKKGWIKIQBEVDDIVQTKVAGGBIVR 235
 Db 209 IGBHDSSPLWGSVNTAVGALKTLDPKLGDSDKEHW-----KTHHQVQISAVEIIK 262

Qy 216 LLGGSSAYXARGASAIQMASLYSLKDRKRVMVCSYLCQGQYQNH-XLGVPCVIGGRGVE 294
 Db 263 LKGYTS--WAIGSMVMDLGSILKLNRLRVHPYSTMVKGLYGKEELFLSIPCVLRGNVGS 320

Qy 295 KITELELTQAEROLQSGTDEVKEMQK 321
 Db 321 DVVKINLNSBEEAFKKSKETLWNIQ 347

RESULT 14
 US-09-7.0-279-1412
 ; Sequence 1412; Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; FILE REFERENCE: PU3480US
 ; TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2384
 ; LENGTH: 322
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-09-710-279-2384

Query Match 23.8%; Score 401.5; DB 2; Length 322;
 Best Local Similarity 29.3%; Pred. No. 2.1e-35;
 Matches 93; Conservative 75; Mis matches 140; Indels 9; Gaps 4;

Qy 11 KIAMVGSIGCTMAFLCSLRELG-D-VVLFDVNPMPKAMDISSHNSSSVVDTGITRVYGS 69
 Db 13 KVVLVGDSGSVGSYAFAMVTOGIADFEVIIAKDKEADYVQLNFGALYSSSPVTV-KA 71

Qy 70 NSYECKGADVVIITAGTIKIPGKSDKEWSBMDLPLWNIKIMBEVGAAIKSYCPNAFVIN 129
 Db 72 GEYEDCKDADLWVITAGAPQKGE----TRQLVKEVNKTLMKSIVTSMDSGFDFFLI 126

Qy 130 ITNPLDWNVAALQESSGLPHHRIGMAGMLSSRFRMIAKDEVSPPDVQGMVIGHGD 189
 Db 127 AANPDILTRIVKEVTLPAARVIGSGTVDLSARFLYLSKELGTVSSVHASTIGEHD 186

Qy 190 HMVPLSLRYATVNGIPLSEFVKKGWIKIQBEVDDIVQTKVAGGEIVRLLGQGSAYYAGAS 249
 Db 187 SELAWMSQANYGGISYDTLKEETGSDAKANEIYINTRDAAYDIIQ--AKGSTYIGIALA 244

RESULT 15
 US-09-7.0-279-2384
 ; Sequence 2384; Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; FILE REFERENCE: PU3480US
 ; TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2384
 ; LENGTH: 322
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-09-710-279-2384

Query Match 23.8%; Score 401.5; DB 2; Length 322;
 Best Local Similarity 29.3%; Pred. No. 2.1e-35;
 Matches 93; Conservative 75; Mis matches 140; Indels 9; Gaps 4;

Qy 11 KIAMVGSIGCTMAFLCSLRELG-D-VVLFDVNPMPKAMDISSHNSSSVVDTGITRVYGS 69
 Db 13 KVVLVGDSGSVGSYAFAMVTOGIADFEVIIAKDKEADYVQLNFGALYSSSPVTV-KA 71

Qy 70 NSYECKGADVVIITAGTIKIPGKSDKEWSBMDLPLWNIKIMBEVGAAIKSYCPNAFVIN 129
 Db 72 GEYEDCKDADLWVITAGAPQKGE----TRQLVKEVNKTLMKSIVTSMDSGFDFFLI 126

Qy 130 ITNPLDWNVAALQESSGLPHHRIGMAGMLSSRFRMIAKDEVSPPDVQGMVIGHGD 189
 Db 127 AANPDILTRIVKEVTLPAARVIGSGTVDLSARFLYLSKELGTVSSVHASTIGEHD 186

Qy 190 HMVPLSLRYATVNGIPLSEFVKKGWIKIQBEVDDIVQTKVAGGEIVRLLGQGSAYYAGAS 249
 Db 187 SELAWMSQANYGGISYDTLKEETGSDAKANEIYINTRDAAYDIIQ--AKGSTYIGIALA 244

Qy 250 AIQMAESYLKDRAKRNWVNCSCYLOGQGVQNHYLGVPCVIGGRGVEKIELELTQAERQEL 309
 Db 245 LRIRSKALLNNENNSILTIVSOLNGQFENDYGLPLTLINQGAVIYETPLNDNEIQLL 304

Db 310 QCSIDEVREMOKAIAL 326
 Db 305 EKSVKTLEDTDSIKHL 321

Search completed: March 2, 2006, 19:41:16
 Job time : 29 secs

Page 1

protein - protein search, using SW model	US-09-390-846-2	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
on: March 2, 2006, 19:38:02 ; Search time 109 Seconds (without alignments)	1688	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
title: BLOSUM62	1 MAVFEKNTRKIAMVGSGMI.....GSTDEVKEMQKAIAALDASK 330	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
Sequence:	Gapop 10.0 , Gapext 0.5	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
oring table:	BLOSUM62	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
searched:	2166443 seqs, 705528306 residues	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
total number of hits satisfying chosen parameters:	2166443	Q8i8u5_EIMAC	Q8i8u5_EIMAC PRELIMINARY;	PRT;	330 AA.
minimum DB seq length: 0		AC	AC	PRT;	330 AA.
maximum DB seq length: 2000000000		DT	DT	PRT;	330 AA.
st-processing: Minimum Match 0%		DT	DT	PRT;	330 AA.
Maximum Match 100%		DT	DT	PRT;	330 AA.
Listing First 45 summaries		DE	DE	PRT;	330 AA.
Database :	UniProt 05.80.*	GN	GN	PRT;	330 AA.
1: uniprot_sprot:*	Q8i8u5_EIMAC	RA	RA	PRT;	330 AA.
2: uniprot_trembl:*	Q8i8u5_EIMAC	RN	RN	PRT;	330 AA.
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		RN	RN	PRT;	330 AA.
SUMMARIES		RN	RN	PRT;	330 AA.
result	%	Query	Description		
No.	Score	Match	Length	DB	ID
1	1688	100.0	330	2	Q8i8u5_EIMAC
2	1398	82.8	330	2	Q8i8u3_EIMMA
3	1266	75.0	331	2	Q8i8u4_EIMTE
4	1072	63.5	326	1	LDH_TOXO
5	1041.5	61.7	329	2	P90613_TOXGO
6	905.5	53.6	316	2	Q6DQL2_TOBGO
7	889	52.7	330	2	Q720X7_BABGO
8	886.5	52.5	320	1	MDH_RHTLV
9	881	52.2	316	2	Q9PRK9_PLAVI
10	877.5	52.0	320	1	MDH_BARBE
11	876.5	51.9	320	1	MDH_BRUME
12	873.5	51.7	320	1	MDH_BRUMET
13	873.5	51.7	320	1	MDH_BRUMET
14	870.5	51.6	320	1	MDH_BARQU
15	868	51.5	320	1	MDH_BRUBA
16	868	51.4	322	1	MDH_BRAJA
17	863.5	51.2	320	1	MDH_BRUSU
18	862.5	51.1	322	1	MDH_BRUSA
19	862.5	51.1	324	2	Q4TP00_9SPHN
20	862	51.1	322	1	MDH_RHTIO
21	851.5	50.4	320	1	MDH_METIX
22	851.5	50.4	320	1	MDH_BRUSA
23	850.5	50.4	320	1	MDH_CAUCR
24	847	50.2	299	2	Q5JH30_PLAVI
25	846.5	50.1	314	1	Q7PBN3_RICSI
26	837.5	49.6	314	1	MDH_RICCN
27	836	49.5	316	2	Q7RHUB_PLAVI
28	835	49.5	299	1	Q6JH31_PLAMA
29	833	49.3	316	2	Q4Z783_PLABE
30	833	49.3	322	1	Q5JH32_PLAPC
31	831.5	49.3	316	1	LDH1_PLAFD
32	831.5	49.3	316	2	Q5R2J8_PLARE
33	831.5	49.3	316	2	Q76NM3_PLAF7
34	831.5	49.3	316	2	Q71T02_PLAFA
35	826.5	49.0	314	1	MDH_RICPR
36	826.5	49.0	314	1	MDH_RICRY
37	824	48.8	316	2	Q4XTG3_PLACH
38	822.5	48.7	314	1	MDH_RICPE
39	810.5	48.0	316	1	MDH_WOLPM
40	808.5	47.9	316	1	LDH_BOCTR
41	808.5	47.9	316	1	MDH_WOLTR
42	807.5	47.8	316	2	Q9BM13_PLAFA
43	807	47.8	299	2	Q5JH32_PLAPC
44	806.5	47.8	317	1	MDH_GEOSL
45	805	47.7	321	2	Q4N61B_THEPA
					ALIGNMENTS

121	YCPNAFVININTNPLDVMVAALQESGLPFRICMAGMJDSSRPRMLADKLEVSPRDVQ	180	Db	181	GMVIGHGDHMPLSRVATYNGIPISSEFYKKWIKQEYEVDDIVQTKTKVAGGETVRLLGCG	240
181	GMVIGHGDHMPLSRVATYNGIPISSEFYKKWIKQEYEVDDIVQTKTKVAGGETVRLLGCG	240	Qy	241	SAYA PGASA IOMAE SYL KDR KRV MWC SCYL QO QY GVN NH LG CP CVIG GR GE YK II E	300
181	GMVIGHGDHMPLSRVATYNGIPISSEFYKKWIKQEYEVDDIVQTKTKVAGGETVRLLGCG	240	Db	241	SAYA PGAS TAI MAE SYL KDR KRL FV S SCYL QO QY GVN NH LG CP CVIG KG GE YK II E	300
241	SAYA PGASA IOMAE SYL KDR KRV MWC SCYL QO QY GVN NH LG CP CVIG GR GE YK II E	300	Qy	301	LTAQERQELQSIDEVKEMOKATAALDA SK	330
241	SAYA PGASA IOMAE SYL KDR KRV MWC SCYL QO QY GVN NH LG CP CVIG GR GE YK II E	300	Db	301	LNQE EKCLLQG SIDEVKEMOKATAALDA SK	330
301	LTAQERQELQSIDEVKEMOKATAALDA SK	330	Qy	RESULT 3		
301	LTAQERQELQSIDEVKEMOKATAALDA SK	330	Db	Q818U4	ETIMTE	
				ID	Q818U4_BIMTE PRELIMINARY;	PRT;
				AC	Q818U4_	331 AA.
				DT	01-MAR-2003 (TREMBUREL.	23; Created)
				DT	01-MAR-2004 (TREMBUREL.	23; Last sequence update)
				DE	01-MAR-2004 (TREMBUREL.	26; Last annotation update)
				GN	Name=Ldh;	
				OS	Bimeria tenella.	
				OC	Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Bimeriidae;	
				OC	Eimeria.	
				OX	NCBI_TaxID=5602;	
				RN	[1]	
				RP	NUCLEOTIDE SEQUENCE.	
				RA	Schaap D.C.;	
				RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.	
				RN	[2]	
				RP	NUCLEOTIDE SEQUENCE.	
				RA	Arce G.; Krozen H.; Schaap D.C.;	
				RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	
				CC	-I- SIMILARITY: Belongs to the LDH/MDH superfamily. LDH Family.	
				DR	EMBL; AY143389; AAN38976.1; -; mRNA.	
				DR	HSSP; 027743; 1CET.	
				DR	GO; GO:0004439; F-L-lactate dehydrogenase activity; IEA.	
				DR	GO; GO:0016451; F:oxidoreductase activity; IEA.	
				DR	GO; GO:0006096; P:glycolysis; IEA.	
				DR	GO; GO:0006100; P:tricarboxylic acid cycle intermediate metab.. . ; IEA.	
				DR	InterPro; IPR01236; 1dh.	
				DR	InterPro; IPK001557; L_LDH_MDH.	
				DR	Pfam; PF02866; Ldh_1_C_1.	
				DR	Pfam; PF00056; Ldh_1_N_1.	
				DR	PRINTS; PIRSF00102; Lac_dehydrog_1.	
				DR	PRINTS; PR00086; LLDHDRGNASE.	
				KW	Oxidoreductase; 331 AA; 34965 MW; BEF87B9F837AE469 CRC64;	
				SQ	SEQUENCE	
					Query Match	75.0%;
					Best Local Similarity	Score 1266; DB 2;
					Matches 235;	Length 331;
					Conservative	Best Local Similarity 71.4%; Pred. No. 9.4e-88;
					Mismatches 51;	Mismatches 43;
					Indels 0;	Gaps 0;
				Qy	1 MAYFEKTRPKIAMVGSMIGGTMAFLCSCSLRELGVDVLFDPVNPMPGMKAMDISHNSVV	60
				Db	1 MAVFEKTRPKIAVGSMIGGTMAFLCSCSLRELGVDVLFDPVNPMPGMKAMDISHNSVV	60
					1 MAVFEKTRPKIAVGSMIGGTMAFLCSCSLRELGVDVLFDPVNPMPGMKAMDISHNSVV	60
				Qy	61 DTGTTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Db	61 DTGTTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Qy	61 DNGT GTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Db	61 DNGT GTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Qy	1 MAVFEKTRPKIAMVGSMIGGTMAFLCSCSLRELGVDVLFDPVNPMPGMKAMDISHNSVV	60
				Db	1 MAVFEKTRPKIAVGSMIGGTMAFLCSCSLRELGVDVLFDPVNPMPGMKAMDISHNSVV	60
					1 MAVFEKTRPKIAVGSMIGGTMAFLCSCSLRELGVDVLFDPVNPMPGMKAMDISHNSVV	60
				Qy	61 DTGTTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Db	61 DTGTTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Qy	61 DNGT GTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Db	61 DNGT GTVYGSNSYECLKGA D VVITAGITIPKGSKDKESMRDLLPVN KIMREVGAAKS	120
				Qy	121 YCPNAFVININTNPLDVMVAALQESGLPFRICMAGMJDSSRPRMIDLKPVN KIMREVGAAKS	120
				Db	121 YCPNAFVININTNPLDVMVAALQESGLPFRICMAGMJDSSRPRMIDLKPVN KIMREVGAAKS	120
				Qy	121 YCPNAFVININTNPLDVMVAALQESGLPFRICMAGMJDSSRPRMIDLKPVN KIMREVGAAKS	120
				Db	121 YCPNAFVININTNPLDVMVAALQESGLPFRICMAGMJDSSRPRMIDLKPVN KIMREVGAAKS	120
				Qy	181 GMVIGHGDHMPLSRVATYNGIPISSEFYKKWIKQEYEVDDIVQTKTKVAGGETVRLLGCG	240
				Db	181 AMVIGHGDHMPLSRVATYNGIPISSEFYKKWIKQEYEVDDIVQTKTKVAGGETVRLLGCG	240
				Qy	241 SAYA PGASA IOMAE SYL KDR KRV MWC SCYL QO QY GVN NH LG CP CVIG GR GE YK II E	300
				Db	241 SAYA PGAS TAI MAE SYL KDR KRL FV S SCYL QO QY GVN NH LG CP CVIG KG GE YK II E	300
				Qy	301 LTAQERQELQSIDEVKEMOKATAALDA SK	330

Db	301 LDAREQLQASIDEVEMIRQLAAADA	329	Db	188 DHMLPLARYTVTSGFPLREFIKGKMTAEKLAETVERTKKAGGEVRLLGQQSYAYAPAL	247
RESULT 4			Qy	249 SAIONDAESTYLIKDKRKRVMVSCYLOGQYGVNHYLGGVPCYTGGRGEVKTELELTQAERQE	308
LDH_TOXGO	STANDARD;	PRT;	Db	248 SAINTAQAFLKDKRVLPSVCIGEYGLHDMPFLGPVAVGGGIEQVIELELTBHQBC	307
ID			Qy	309 LOGSDEVEMOKAIAL	326
AC Q27797; DT 01-NOV-1997 (Rel. 35, Created)			Db	308 FRKSVDVVELNRKSLAAL	325
DT 01-NOV-1997 (Rel. 35, Last sequence update)					
DT 13-SEP-2005 (Rel. 48, Last annotation update)					
DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH).					
OS Toxoplasma gondii.					
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;					
OC Toxoplasma.					
OX NCBI_TAXID=5811;					
RN [1]					
NUCLEOTIDE SEQUENCE.					
STRAIN=Me49;					
RX MEDLINE=86123406; PubMed=8577343; DOI=10.1016/0166-6851(95)00069-D;					
RA Yang, S.; Parmley, S. F.;					
RT "A bradyzoite stage-specifically expressed gene of Toxoplasma gondii encodes a polypeptide homologous to lactate dehydrogenase.";					
RT Mol. Biochem Parasitol. 73:291-294 (1995).					
RL					
CC - - PATHWAY: Anaerobic glycolysis; final step.					
CC - - SUBUNIT: Homotetramer (By similarity).					
CC - - SIMILARITY: Belongs to the LDH/MDH superfamily. LDH Family.					
CC					
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CC					
EMBL; U23207; AAC48863.1; mRNA.					
DR 1SOV; X-ray; A/B=1-326.					
PDB; 1SOV; X-ray; A/B=1-326.					
DR 1SPW; X-ray; A/B=1-326.					
SMR; Q27797; 3-325.					
DR InterPro; IPR011304; L-LDH-NAD.					
DR InterPro; IPR001557; L-LDH_MDH.					
DR InterPro; IPR001236; 1dh.					
DR PANHER; PTHR11540; 1dh.					
DR Pfam; PF02866; Ldh_1_C; 1.					
DR Pfam; PF00056; Ldh_1_N; 1.					
DR PIRSF; PIRSF00102; Lac_mal_DH; 1.					
DR PRINTS; PR00086; LDHDHRNASE.					
DR PROSITE; PS00064; L-LDH; FALSE_NEG.					
KW 3D-structure; Glycotysis; NAD; Oxidoreductase.					
NP BIND 39 60 NAD (By similarity).					
FT ACT SITE 186 186 Proton acceptor (By similarity).					
FT BINDING 99 99 Substrate (By similarity).					
FT BINDING 131 131 NAD or substrate (By similarity).					
FT BINDING 162 162 Substrate (By similarity).					
SQ SEQUENCE 326 AA; 35307 MW; E69295A81FC031E CRC64;					
Query Match 63 5%; Score 1072; DB 1; Length 326;					
Best Local Similarity 62 6%; Pred. No. 4.9e-73; Indels 0; Gaps 0;					
Matches 199; Conservative 56; Mismatches 63; Indels 0; Gaps 0;					
Qy 9 RPKIAMVGSGMIGGTMAFLCSLRELGDVWLFDVYPNMNGKAMPDISHNSVWDGIRTYG 68					
Db 8 RKKZAMIGSGMIGGTMGYCLVTLRELAADVLFDVUTGMPKGAKLDSQATSIADINVSTY 67					
Qy 69 SNSYECYLKGADVVITTAGITKIPGKSDKEMSRMIDLPPVNIKIMREVGAIAKSYCPNAFTVI 128					
Db 68 ANQYKIAASGDVVITAGITKVPGKSDKEMSRNDLPPFAKTIREVQAVKKYCPPLAVFTI 127					
Qy 129 NITNPLDVMVTAALQBSSGLPHHRICGMAGMLDSSRFMIAKLEVSFRDVGQMVIGYHG 188					
Db 128 VVTNPLDCMKVCFHEASGLPKNMVCGMANVLSARFRRIADOLEISPRDIQATVIGHG 187					
Qy 189 DMMYPLSRVATVNGIPLSBSFKKGWIQOBEVDDIVQKTRVAGGBIVRLJGQQGSAYAYPA 248					
Db 129 IVVTPNPLDMVVKMCASGVPNNICGACMJDGSRFRRYVADLSVSPRDVATVIGH 188					
Qy 188 GDHMVPLSRVATVNGIPLSBSFKKGWIQOBEVDDIVQKTRVAGGBIVRLJGQQGSAYAYPA 247					
Db 189 GDCMVPVRYITVNGPIQKFIRDGWVTEKOLBEIAEHTKVSCEGEIVRFLGQQGSAYAYPA 248					
Qy 248 ASATQMASYSLKDRKRVNVCSCYLGQYGVQNEYLGQYGVIGERGVKEJIELELTQPRQ 307					

Page 6

DB	63	ANDYAAIEGADVIVITAGVPRKPG-----MSRDLILGINLKMEQVGAGTKKYAPEAFVU	117	DR PIR: AF2900; AF2900.
DR	129	NITNPDLDMVTAALQESSGLPHHRICMAGILDSSPRMADKLEVSPPDVQGMVIGVHG	188	DR PIR: G97675; G97675.
Qy	118	CITNPLDAMWALQKFSGLPAHKVGMAGLVDSSARTERYFSEEFTNSVEDTAFVLGGHG	177	DR HSSP: P80010; 1GUY.
Db	189	DHMPBLRSRATVNGIPLSSETVKGNTIKOBEYDIVTKYAGGETIVRLLOGGSAYTAPGA	248	DR HAMPA: MF 00487; -; 1.
Qy	178	DSMPYLARSTVAGIPLSLDKYMGWTSDQEDKTIORTRGDAEVGLLTGSAFTAPAA	237	DR InterPro: IPR01557; L_LDH_MDH.
Db	249	SATQNAEAVSILKDRKVMWCSCLQGQGYGVNQHLYGCPVCVGGRYVEKILEELTAQEROE	308	DR InterPro: IPR01236; 1Dh.
Qy	238	SATQNAEAVSYRKDKRVLVLPVAQSLSGXGVMDMVYGVPTVIGANGVERIEBIDLDKDEAQ	297	DR InterPro: IPR011275; MalatedH_bact.
Db	309	LOGSIDEDEVKMQATAALDAS	329	DR PANTHER: PTHR11540; 1Dh.
Qy	MDH_AGR75	STANDARD;	PRT;	320 AA.
AC	07CWK7; Q8UC59;			DR Pfam: PF02865; Ldh_1_C; 1.
DT	25-OCT-2004 (Rel. 45, Created)			DR PRINTS: PRO0086; Ldh_1_N; 1.
DT	25-OCT-2004 (Rel. 45, Last sequence update)			DR TIGRFAMS: TIGR01763; MalatedH_bact; 1.
DE	Malate dehydrogenase			DR Proton relay (By similarity).
GN	Name=mdh; OrderedLocusNames=Atu2619; AGR_C:4782;			DR Proton relay (By similarity).
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).			DR Substrate carboxyl (By similarity).
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			DR Substrate carboxyl (By similarity).
NCBI_TaxID	176299;			DR Substrate carboxyl (By similarity).
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			DR PRINTS: PRO0086; CRC64; 1.
RX	MEDLINE=1608850; PubMed=11743193; DOI=10.1126/science.1066804;			DR PRINTS: TIGR01763; MalatedH_bact.
RA	Wood D.W., Setubal J.C., Kaufl R., Monks D.P., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boree D. Sr., Chapman P., Clendinnen J., Deatherage G., Gillette W., Grant C., Kurayavin T., Levy R., Li M.-J., McClelland B., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Raymond S., Yoo H., Tao Y., Bidle D., Jung M., Krueger W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.,			DR PRINTS: TIGR01763; MalatedH_bact.
RA	"The genome of the natural genetic engineer Agrobacterium tumefaciens C58."			DR PRINTS: TIGR01763; MalatedH_bact.
RT	Science 294:2317-2323 (2001).			DR PRINTS: TIGR01763; MalatedH_bact.
RN	[2]			DR PRINTS: TIGR01763; MalatedH_bact.
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			DR PRINTS: TIGR01763; MalatedH_bact.
RX	MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;			DR PRINTS: TIGR01763; MalatedH_bact.
RA	Goodner B., Hinkie G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askewazi M., Halling C., Mullin L., Houmell K., Gordon J., Vaudin M., Tarchtchou O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markez B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., "Slatier S,"			DR PRINTS: TIGR01763; MalatedH_bact.
RA	"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."			DR PRINTS: TIGR01763; MalatedH_bact.
RT	Science 294:2323-2328 (2001).			DR PRINTS: TIGR01763; MalatedH_bact.
RN	[1]			DR PRINTS: TIGR01763; MalatedH_bact.
CC	-1 - FUNCTION: Catalyzes the reversible oxidation of malate to oxaloacetate (By similarity).			DR PRINTS: TIGR01763; MalatedH_bact.
CC	-1 - CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.			DR PRINTS: TIGR01763; MalatedH_bact.
CC	-1 - SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.			DR PRINTS: TIGR01763; MalatedH_bact.
CC	This Swiss-Prot entry is Copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			DR PRINTS: TIGR01763; MalatedH_bact.
CC	CC NUCLEOTIDE SEQUENCE.			DR PRINTS: TIGR01763; MalatedH_bact.
CC	RA Dymov S.I., Meek D.J., Driscoll B.T.;			DR PRINTS: TIGR01763; MalatedH_bact.
CC	RT "Isolation of a malate dehydrogenase mutant and genes encoding a putative TCA cycle operon of Sinorhizobium meliloti."			DR PRINTS: TIGR01763; MalatedH_bact.
CC	RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			DR PRINTS: TIGR01763; MalatedH_bact.
CC	RL STRAIN=1021;			DR PRINTS: TIGR01763; MalatedH_bact.
CC	RN			DR PRINTS: TIGR01763; MalatedH_bact.
CC	RP GENOMIC DNA.			DR PRINTS: TIGR01763; MalatedH_bact.
CC	EMBL; ARGO0211; AR043620.1;			DR PRINTS: TIGR01763; MalatedH_bact.
CC	EMBL; AE008177; AR883360.1;			DR PRINTS: TIGR01763; MalatedH_bact.
CC	DR			DR PRINTS: TIGR01763; MalatedH_bact.

RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;	ID MDH_BARQU	STANDARD; PRT; 320 AA.
RA Capela D., Barloy-Hubert F., Gouy J., Boite G., Ampe F., Batut J.,	AC Q6FYD0;	Created
RA Boulard P., Becker A., Bourry M., Cadiou E., Dreano S., Gloux S.,	DT DT 25-OCT-2004 (Rel. 45, Last sequence update)	
RA Goorie T., Goffeau A., Kahn D., Kiss B., Lelauré V., Masuy D.,	DT DT 13-SEP-2005 (Rel. 48, Last annotation update)	
RA Pohl T., Portetelle D., Puellet A., Purnelle B., Ransperger U.,	DE Malate dehydrogenase (EC 1.1.1.37)	
RA Renard C., Thebaud P., Vandebol M., Weidner S., Galibert F.;	GN Name=mdh; OrderedLocusName=BQ1-1450;	
RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."	OS Bartonella quintana (Rochalimaea quintana)	
RT Prok. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).	OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;	
RL Bartonellaceae; Bartonella.	OC NCBI_TAXID=803;	
CC [1] - TAXID=803;	OX RN [1] -	
CC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP STRAIN=Toulouse;	
CC PubMed=15210978; DOI=10.1073/pnas.0305659101;	RC RX	
CC Alsmark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H.,	RA Canbaek B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,	
CC "The louse-borne human pathogen Bartonella quintana is a genomic derivative of the zoonotic agent Bartonella hanseleae."	RA La Scola B., Holmberg M., Andersson S.G.E.;	
CC Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).	RT RT	
CC - - FUNCTION: Catalyzes the reversible oxidation of malate to oxaloacetate (By similarity).	RL LDH	
CC - - CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.	CC CC	
CC - - SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.	CC CC	
CC EMBL; AL591792; CAC47635.1; -; Genomic_DNA.	CC CC	
CC HSSEP; PR0040; 1GUY.	CC CC	
CC HAMAP; MF_00487; -; 1.	CC CC	
CC InterPro; IPR011557; L_LDH_MDH.	CC CC	
CC InterPro; IPR011236; Idh.	CC CC	
CC InterPro; IPR011232; Mdh_AS.	CC CC	
CC InterPro; PTHR11540; 1dh.	CC CC	
CC InterPro; PTHR11540; 1dh.	CC CC	
CC InterPro; PR02866; Ldh_1_C; 1.	CC CC	
CC Pfam; PF0056; Ldh_1_N; 1.	CC CC	
CC Pfam; PF0056; Ldh_1_N; 1.	CC CC	
DR PRINTS; PRRSF00102; Lac_mal_DH; 1.	CC CC	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	CC CC	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	DR DR	
FT ACT SITE 176 176 Proton relay (By similarity).	DR DR	
FT BINDING 83 83 Substrate carboxyl (By similarity).	DR DR	
FT BINDING 89 89 Substrate carboxyl (By similarity).	DR DR	
FT BINDING 152 152 Substrate carboxyl (By similarity).	DR DR	
SQ SEQUENCE 320 AA; 33611 MW; 3CPI14C7211F9FA CRC64;	DR DR	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 152 152 Substrate carboxyl (By similarity).	FT FT	
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Matches 167; Conservative 63; Mismatches 79; Indels 5; Gaps 1;	DR DR	
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KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 152 152 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
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Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
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Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
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Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
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FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
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FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
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Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
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FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
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FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
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FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
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Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
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Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR PRINTS; PR00086; LDHDGRNASE.	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	
DR SEQUENCE 320 AA; 33935 MW; 5ABD8A64348D544 CRC64;	DR DR	
Query Match 51.6%; Score 870.5; DB 1; Length 320;	DR DR	
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;	DR DR	
DR TIGRFAMS; TIGR01763; MalateDH_bact; 1.	DR DR	
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.	DR DR	
FT ACT SITE 149 149 Proton relay (By similarity).	FT FT	
FT ACT SITE 176 176 Proton relay (By similarity).	FT FT	
FT BINDING 83 83 Substrate carboxyl (By similarity).	FT FT	
FT BINDING 89 89 Substrate carboxyl (By similarity).	FT FT	

Qy 249 SAIONAESTYLKDRKRMVMSCYLOGQYGVNHYLGVPCVIGGRGEVKILEELTAQEROE 308
 Qy 238 SAISNAEAETLKDGRVVPATIVLSEBYGVRDTIVGVPVVLGAGSVERVIEIDDKERSA 297
 Qy 309 LOGSTDEVKEMOKATAAL 326
 Db 298 FEQSYNAVKLCEACTAI 315

RESULT 15

MDB_BRUB ID MDB_BRUB STANDARD; PRT; 320 AA.
 AC Q57AX1;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Malate dehydrogenase (EC 1.1.1.37).
 GN Name=mdh; OrderedLocusNames=BruAbI_1903;
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 NCBI_TaxID=235;

RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=9-941 / Bovar 1;
 RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
 RA Halling S.M., Peterkin-Burck B.D., Bricker B.J., Zuerner R.L.,
 RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
 RT "Completion of the genome sequence of *Brucella abortus* and comparison
 to the highly similar genomes of *Brucella melitensis* and *Brucella
 suis*";
 RT J. Bacteriol. 187:2725-2726(2005).
 CC -I- FUNCTION: Catalyzes the reversible oxidation of malate to
 oxaloacetate (By similarity).
 CC -I- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
 CC -I- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.

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CC DR EMBL: AFB17223; APX7213.1; -; Genomic_DNA.
 DR HAMAP; MR_00487; MR_1_N; 1.
 DR InterPro; IPR001527; L LDH_MDH.
 DR InterPro; IPR001236; 1dh.
 DR InterPro; IPR011205; MalatedH_bact.
 DR PANTHER; PTHR11540; 1dh.
 PFam; PF02866; Ldh_1_C; 1.
 DR PF00056; Ldh_1_N; 1.
 DR PIRSF; PIRSF00010; Lac_mal_DH; 1.
 DR PRINTS; PR00086; LLDHDRGNASE.
 DR TIGR01763; MalatedH_bact; 1.
 KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.
 FT ACT_SITE 149 149 Proton relay (By similarity).
 FT BINDING 176 176 Substrate carboxyl (By similarity).
 FT BINDING 83 83 Substrate carboxyl (By similarity).
 FT BINDING 89 89 Substrate carboxyl (By similarity).
 FT BINDING 152 152 Substrate carboxyl (By similarity).
 SQ SEQUENCE 320 AA; 33704 MW; C212BA8F0241677 CRC64;

Query Match 51.5%; Score 86.5; DB 1; Length 320;
 Best Local Similarity 53.9%; Pred. No. 1.4e-57;
 Matches 173; Conservative 53; Mismatches 90; Indels 5; Gaps 1;

Qy 9 RPKIAMVGGMIGGTMAFFLCSLRFLGDLVTFDLYVPPNMKGAMDISHNSSVVTGTRVY 68
 Db 3 RNKALIGGMIGETLAAJAGLRELGDVFLFDIAEGTQGKGDIABESPVDGFDAREFTG 62

Qy 69 SNSYECLKCADWVITAGITKIPKSDEWSRMDLLPTNIMREVAKSKYCPNMFV 128

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Copyright (c) 1993 - 2006	GenCore version 5.1.7	
OM protein - protein search, using sw model		
Run on:	March 2, 2006, 19:38:27 ;	Search time 24 Seconds (without alignments)
Title:	US-09-390-846-2	1322.980 Million cell updates/sec
Perfect score:	1688	
Sequence:	1 MAVFEKNTRPIAMVSGMI.....GSIDEVKEMQKAIAALDASK 330	
Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Searched:	283416 seqs, 96216763 residues	
Total number of hits satisfying chosen parameters:	283416	

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query Match	Length	DB ID	Description
1	876.5	51.9	326	2 AD3269	malate dehydrogena
2	873.5	51.7	320	2 AF2900	malate dehydrogena
3	873.5	51.7	352	2 G97675	malate dehydrogena
4	850.5	50.4	320	2 B87702	malate dehydrogena
5	827.5	49.6	314	2 H97764	malate dehydrogena
6	826.5	49.0	314	2 A71695	malate dehydrogena
7	740	43.8	312	2 I40383	malate dehydrogena
8	729	43.2	312	2 S61213	malate dehydrogena
9	709	42.0	314	2 F84044	probable malate de
10	634	37.6	324	2 S75735	malate dehydrogena
11	605.5	35.9	335	2 E70453	malate dehydrogena
12	559	33.7	334	2 D70444	malate dehydrogena
13	566.5	33.6	284	2 AC2346	probable malate de
14	560.5	33.2	313	2 H72655	L-lactate dehydrogena
15	478	28.3	314	2 H86671	L-lactate dehydrogena
16	465.5	27.6	313	2 AC1463	L-lactate dehydrogena
17	463.5	27.5	313	2 AC1101	L-lactate dehydrogena
18	460	27.3	321	2 E69649	L-lactate dehydrogena
19	455	27.0	318	1 DEBSLM	L-lactate dehydrogena
20	454	26.9	313	2 E96932	L-lactate dehydrogena
21	440.5	26.1	353	2 F71447	L-lactate dehydrogena
22	440	26.1	318	2 S08182	L-lactate dehydrogena
23	439.5	26.0	319	2 S36863	L-lactate dehydrogena
24	434.5	25.7	312	2 H64250	L-lactate dehydrogena
25	431.5	25.6	326	1 DEBLA	L-lactate dehydrogena
26	431	25.5	319	2 S08183	L-lactate dehydrogena
27	428	25.4	317	2 B29704	L-lactate dehydrogena
28	424.5	25.1	317	2 S00019	L-lactate dehydrogena
29	423.5	25.1	320	2 JQ0183	L-lactate dehydrogena

ALIGNMENTS

RESULT 1	AD3269	malate dehydrogenase (EC 1.1.1.37) [imported] - <i>Brucella melitensis</i> (strain 16M)
C;Species:	Brucella melitensis	
C;Date:	01-Feb-2002	#sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession:	AD3269	
R;DeVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Muier, C.; Los, T.; Ivanova, T.; Mazur, M.; Goitsman, E.; Selkov, E.; Eizer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, A;Title: The genome sequence of the facultative intracellular pathogen <i>Brucella melitensis</i> A;Reference number: AD3252; PMID:11756688		
A;Status: preliminary		
A;Map type: DNA		
A;Residues: 1-326 <KUR>		
A;Cross-references: UNIPARC:UPI0000057B76; GB:AE008917; PIDN:AAL51319.1;		
A;Experimental source: strain 16M		
C;Genetics:		
A;Gene: BMEI0137		
A;Map position: I		
C;Superfamily: L-lactate dehydrogenase		
C;Keywords: oxidoreductase		
Query Match	51.9%	Score 876.5; DB 2; Length 326;
Best Local Similarity	54.2%	Pred. No. 8e-60; Mismatches 89; Indels 5; Gaps 1;
Matches 174; Conservative Matches 174; Cross-references: UNIPARC:UPI0000057B76; GB:AE008917; PIDN:AAL51319.1;		
QY 9 RPKIAVMGSGMGCTMAFLCSURELGDVYLFDVVPNMPMGKAMDISHNSSSVVDTGIVTYVG 68		
9 RNKIALIGSGMGITLAHLAGLKLPGDKGQDGKJLAEESPVDGDKATGTG 68		
Db 69 SNSYECILKGADWVYTITAGTGTIPKPKSDKEWSRMDLPYNIKIMREVGAIAKSKYCPNAFVTI 128		
69 ANDYAIEGADWVYTATGVPKRKG----MSRDDLGLNLKMEQVGAGIKCYAPEAFVTI 123		
QY 129 NITNPDLDMVAALQBSGLPFLPHRICGMAGMLDSRFRMIAKDLKLEVSPPDVQGMVIGVHG 188		
124 CITNPDLDMWAQKFSGPAPKTVGAGLQVLSLKVNGWTSQKLDKIQRTQDGGABIVGLKJTGSAFVPA 183		
Db 189 DHMVLPLSRYATVNGIPLSEFVRKKWIKOBEVDDIVQKTKVAGGEVTRUJGQGSAYAYPA 248		
184 DSMVPLARISTVAGIPLSLVKGWTSQKLDKIQRTQDGGABIVGLKJTGSAFVPA 243		
QY 249 SATQMAESYLKDRIKRVMNCSCYLOGQXGVNHYLGVPVCIGGRGVKEKIELETQERQE 308		
244 SATQMAESYLKDCKRKVLPVAAQLSGGQYKDMVYGPVTVANGVERIEIDLRDEKAQ 303		
Qy 309 LQGSIDEVKEMQKAIALLDAS 329		
Db 304 FDKSVASVAGLCEACIGIAPS 324		

RESULT 2	
AF2900	malate dehydrogenase mdh [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens	
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004	
C;Accession: AF2900	
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L.; George, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.	
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.	
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.	
A;Reference number: AB2577; MUID:21608550; PMID:11743193	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-320 <KUR>	
A;Cross-references: UNIPROT:Q8UCS9; UNIPARC:UPI000016474B; GB:AE008688; PIDN:AAL43620.1;	
A;Experimental source: strain C58 (Dupont)	
C;Genetics:	
A;Gene: mdh	
A;Map position: circular chromosome	
C;Superfamily: L-lactate dehydrogenase	
Query Match	51.7%; Score 873.5; DB 2; Length 352;
Best Local Similarity	51.7%; Pred. No. 1.5e-59;
Matches	167; Conservative 60; MisMatches 82; Indels 5; Gaps 1;
Db	
Qy	9 RPKIAMVGGMIGGTMAFLCSLRELGDVVLFDVVPNNPMGKAMDISSHSSVVDTGITYG 68
Db	35 RKKIAKGAGMIGGTMAFLCSLRELGDVVLFDVVPNNPMGKAMDISSHSSVVDTGITYG 94
Qy	69 SNSYECLKAGDVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAIAIKSYCPNAFVI 128
Db	95 ASDYAAEGADCVTAVKPG----MSRDLGLNLKMEQVGAKKYAPNAFVI 149
Qy	129 NITNPLDMVAALQESSLPHHRICGMGLDSRFRMIAKLEVSPRDVGMLVSPDQGMVLTGVHG 188
Db	150 CTTNPDLDMVAWLQKFSGLPLKNVKVNGAQLDSARFLFLABEENVSQDVTAFLVGLGHG 209
Qy	189 DHMVPRLSRYATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGCGSAYAYPAGA 248
Db	210 DTMVPLARYSTVGGPVLTDLVKMGWTAERLQQITQTRDGAEVLSLKTSSAYYPPA 269
Qy	249 SAQMAESYLDKDRVMVNCSCYLGQGQVNHLYGPVCVIGRGVKEVILTLTAQERQE 308
Db	270 SAQMAESYLDKDRVLPAAAHLSGQVGDMMVGVPTIIGAGGIERVIEELNKEEEAA 329
RESULT 4	
Query Match	51.7%; Score 873.5; DB 2; Length 320;
Best Local Similarity	53.2%; Pred. No. 1.3e-59;
Matches	167; Conservative 60; MisMatches 82; Indels 5; Gaps 1;
Db	3 RKKIALIGSMIGGTMAFLCSLRELGDVVLFDIADGIPGKGLDIAQSCPVEFNAKLGS 62
Qy	69 SNSYECLKAGDVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAIAIKSYCPNAFVI 128
Db	63 ASDYAAEGADCVTAVKPG----MSRDLGLNLKMEQVGAKKYAPNAFVI 117
Qy	129 NITNPLDMVAALQESSLPHHRICGMGLDSRFRMIAKLEVSPRDVGMLVSPDQGMVLTGVHG 188
Db	118 CTTNPDLDMVAWLQKFSGLPLKNVKVNGAQLDSARFLFLABEENVSQDVTAFLVGLGHG 177
Qy	189 DHMVPRLSRYATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGCGSAYAYPAGA 248
Db	178 DTMVPLARYSTVGGPVLTDLVKMGWTAERLQQITQTRDGAEVLSLKTSSAYYPPA 237
Qy	249 SAQMAESYLDKDRVMVNCSCYLGQGQVNHLYGPVCVIGRGVKEVILTLTAQERQE 308
Db	238 SAQMAESTVLDKDRVLPAAAHLSGQVGDMMVGVPTIIGAGGIERVIEELNKEEEAA 297
Qy	309 LGSIDEVEMQKA 322
Db	298 FQKSVGAVAGLCEA 311
Query Match	50.4%; Score 850.5; DB 2; Length 320;
Best Local Similarity	50.1%; Pred. No. 7.7e-58;
Matches	164; Conservative 60; MisMatches 92; Indels 5; Gaps 1;
Db	
Qy	9 RPKIAMVGGMIGGTMAFLCSLRELGDVVLFDVVPNNPMGKAMDISSHSSVVDTGITYG 68
Db	3 RAKIALIGMIGGTMAFLCSLRELGDVVLFDIAGTPQKALDIAEASAVGKDVALKG 62
Qy	69 SNSYECLKAGDVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAIAIKSYCPNAFVI 128
Db	63 ANDYADLAGADCVTAVKPG----MSRDLGLNLKMEQVGAKKYAPNAFVI 117
Qy	129 NITNPLDMVAALQESSLPHHRICGMGLDSRFRMIAKLEVSPRDVGMLVSPDQGMVLTGVHG 188
Db	118 CTTNPDLDMVAWLQKFSGLPLKNVKVNGAQLDSARFLFLABEENVSQDVTAFLVGLGHG 177
Qy	189 DHMVPRLSRYATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGCGSAYAYPAGA 248
Db	178 DTMVPLARYSTVGGPVLTDLVKMGWTAERLQQITQTRDGAEVLSLKTSSAYYPPA 237
Qy	249 SAQMAESYLDKDRVMVNCSCYLGQGQVNHLYGPVCVIGRGVKEVILTLTAQERQE 308
Db	238 SAQMAESTVLDKDRVLPAAAHLSGQVGDMMVGVPTIIGAGGIERVIEELNKEEEAA 297
Qy	309 LGSIDEVEMQKA 322
Db	298 FQKSVGAVAGLCEA 311
RESULT 3	
G97675	malate dehydrogenase [Imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens	
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004	
C;Accession: G97675	
R;Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001	
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens	
A;Accession: G97675	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-352 <KUR>	
A;Cross-references: UNIPROT:Q8UCS9; UNIPARC:UPI00000D1F8D; GB:AE007869; PIDN:AAL4360.1;	
C;Genetics:	
A;Gene: C4782	
A;Map position: circular chromosome	

Db	238 SATAMATSYKDKCRVLPATYLQYQGNDLYTGVVIGAGGAEKIVEFETNDDERAM	297	C;Genetics: A;Gene: mdh; RP376 C;Superfamily: L-lactate dehydrogenase
Qy	309 LOGSIDEVERMORATAALIAS	329	Query Match 49.0%; Score 826.5; DB 2; Length 314; Best Local Similarity 49.8%; Pred. No. 5.3e-56%; Matches 157; Conservative 70; Mismatches 81; Indels 7; Gaps 2;
Db	298 FAKSVESVGLMEACKAIDSS	318	
RESULT 5			
Qy	H97764	5 EKNTRPKIAMVGGMMIGTGMAFLCSLRLRGLDVVLFVPPNMPCGKAMDISHNSVVDPFGI 64	
		65 TYYGDSVYCLKGADWVITAGITIKPERSRMDLPPNINKREVGAAIKSYCPN 124	
		60 KIKGTDYXRDIESDAVITAGLPRKPG ---MSRDLISNTKIMKDVAQNKYQAQN 114	
		125 AFVINTINPLDVMVVAALOESSGLPHHRICGMAGMLDSSRFRMIAKDLKLVSPRDVOGMVI 184	
		115 AFVITINPLDVMVYMLKESGPFLHNCVGMAGLSDRSRFNLFLAKEFVKSVQVNNSVVL 174	
		185 GIVGDHMYPLSRVATVNGIPSEFKCGMIKQBEVDDIVQTKVAGGBIVRLQGSAYY 244	
		175 GHGSDTMPLRISTISGPVPLDGMGLSSNKKNEKIDRTKGNGGGIVKULKTGSAYY 234	
		245 ARGASIAESTLKDRAKRVMVCSCLGQYQVQHLYGVPVCVGEVKEKIBELTAQQ 304	
		235 APASAIAMLESLKDRCQILTCRQVLTQAYLGEYDHLYGVPITIGKEGVIVTELQLEE 294	
		305 ERQELQGSDIDEVKEM 319	
		295 EKILFYKSIVTEVKL 309	
RESULT 7			
Db	11 KIANVGSNIGGGINAAMPLCSURELGDVLDIVPVPNNPMGKAMDISHNSVSVDTGILTGVGSN 70	140383	A;Cross-references: UNIPARC:UPI0000608B0; EMBL:U05257; PID:91045295; PIU C;Species: Bacillus subtilis
Qy	6 KISLIGSGNIGGTIAHLISIRELGDVLDIVPVPQKALDLMQAGTDIKGTN 65	Db	C;Accession: 140383; B69600
Qy	71 SYECIHKADVVITAGITIKPGRKSDKENEWSRMDLPPNINKREVGAAIKSYCPNAFTNI 130	Qy	J; Bacteriol. 176: 4659-4679, 1994
Db	66 DYKDEJGSDAIIITAGLPRKPG ---MSREDLISNTGKTVAAVVKYAPDAFVIVI 120	Db	A;Title: Identification of two distinct <i>Bacillus subtilis</i> citrate synthase genes.
Qy	131 TNPLDVMVVAALOESSGLPHHRICGMAGMLDSSRFRMIAKDLKLVSPRDVOGMVI 190	Db	A;Reference: I40379; MUID:94321340; PMID:8045898
Db	121 TNPLDVMVYMLKESGPFLHNCVGMAGLSDRSRFNLFLAKEFVKSVQVNNSVVLQHGDIA 180	Qy	A;Accession: I40383
Qy	191 MVPLSRVATVNGIPSEFKCGMIKQBEVDDIVQTKVAGGBIVRLQGSAYVAGASA 250	Db	A;Status: preliminary; translated from GB/EMBL/DDJB A;Molecule type: DNA A;Residues: 1-312 -RES-
Db	181 MVPLARYSTSISGVPIPDLKMGSSLNNENLEKIDRTRNGGIEVALLKTGSAYVAPASA 240	Qy	A;Cross-references: UNIPROT:P49814; UNIPARC:UPI0000608B0; EMBL:U05257; PID:91045295; PIU R;Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, G.; Azevedo, V.; Bertler, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Ermenson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; R;In, S.; Sonenshein, A.L.
Qy	251 IOMAESYLKDRCRVMVCSCLGQYGVNHYLGPVCIGRGYEKIKIITLTAQEROQL 310	Db	Nature 390, 249-256, 1997
Db	241 IEMELESYLDKRDQILTCAAHLQGEYGVHDLVYGVPIIMGKEGVLRVIEQLTABEKALED 300	Qy	A;Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleric iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hollsappel, S.; Hosono, S.; Hull, O., M.F. Koettner, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Carter, N.M.; Choi A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauze, Y.M.; Ogawa, K.; Ogivara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon, A.; Serov, A;Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Setkowska, A.; Uchiyama, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yoshiida, K. A;Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
Qy	311 GSIDEVKENQKAI 323	Db	A;Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . A;Reference number: A69580; MUID:9804033; PMID:9384377
Db	301 KSVEGVKLIETI 313	Qy	A;Accession: B69600
RESULT 6			
Qy	A71695	R;Anderson, S.G.E.; Zomordipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, C;Species: <i>Rickettsia prowazekii</i>	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
		C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004	A;Experimental source: strain not shown
		C;Accession: A71695	A;Molecule type: DNA
		R;Anderson, S.G.E.; Zomordipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, C;Species: <i>Rickettsia prowazekii</i>	A;Genetics:
		C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004	A;Gene: citH
		C;Accession: A71695	C;Superfamily: L-lactate dehydrogenase
		A;Status: preliminary; nucleic acid sequence not shown; translation not shown	A;Cross-references: UNIPARC:UPI0000608B0; GB:Z99118; PID:92635200; PIDN:CA
		A;Residues: 1-314 <AND>	A;Cross-references: UNIPROT:Q9ZDF3; UNIPARC:UPI000012BE51; GB:AJ235269; NIH
		A;Experimental source: strain Madrid E	

C;Keywords: oxidoreductase				
Query Match 43.8%; Score 740; DB 2; Length 312;	Qy 7 NTRPIAMVSGMIGGTMAFLCSLRELGVVLFDV--VNMPMGKAMDISHNSVVDTG 64	Oy 307 QEQLOGSIDEVKEMOKAI 323		
Best Local Similarity 45.9%; Pred. No. 2.3e-49;	Db 3 NTRPKVSVAGFEGATTFLAKKEKLAKVVLDFIPQENPTKGAKDLMLEASPVQGEDA 62	Db 295 AAUJKSAESVRNVMKAI 311		
Matches 147; Conservative 63; Mismatches 98; Indels 12; Gaps 3;				
	RESULT 9			
	F84044 malate dehydrogenase citrate [imported] - <i>Bacillus halodurans</i> (strain C-125)			
	C;Species: <i>Bacillus halodurans</i>			
	C;Date: 01-Dec-2000 #text_change 09-Jul-2004			
	C;Sequence_revision 01-Dec-2000			
	C;Accession: F84044			
	R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirai, N.; Masui, N.			
	Nucleic Acids Res., 28, 4317-4331, 2000			
	A;Title: Complete genome sequence of the alkaliphilic bacterium <i>Bacillus halodurans</i> and its draft genome sequence			
	A;Reference number: A83650; MUID:205125B2; PMID:11058132			
	A;Status: Preliminary			
	A;Molecule type: DNA			
	A;Cross-references: UNIPROT:Q9K849; UNIPARC:UPI000012EE31; GB:AP001517; GB:BA000004; NID: 1048			
	A;Experimental source: strain C-125			
	A;Gene: citH			
	C;Superfamily: L-lactate dehydrogenase			
	Query Match 42.0%; Score 709; DB 2; Length 314;			
	Best Local Similarity 44.0%; Pred. No. 5.6e-47;			
	Mismatches 67; Indels 14; Gaps 4;			
	Db 140; Conservative 67; Mismatches 97;			
	Query 9 RPKIAMVSGMIGGTMAFLCSLRELGVVLFDVPM--PMNGKAMDISHNSVVDTG 65			
	Db 5 RRKVSVAGFEGATTFLAKKEKLAKVVLDFIPQENPTKGAKDLMLESPVQGDVN 63			
	66 VYGSNSYECLKGADVVITAGITKIPGKSDKEWSRMDDLPVNKIMREVGAAIKSYCPNA 125			
	Db 64 RTGTSSEYTKDSDVVTAGIARKPG---MSRDDLVTAGIMKAVTREVKGSPNA 118			
	126 FVINTNPFLDNVVAALQESSGLPFRHICGMAGMDSRRMERRMJDKILEVSPRDVQMVIG 185			
	Db 119 YIVVLTNEPADANTTYKESGPKNRTQGSEVLTARFRITVAQEINLSVEDITGVVLG 178			
	Query 186 VRCDHMMPLRSRATVNGIPLSEFKVGMWIKQSEEVDDIVQTKVAGGEVRLLGQSAYA 245			
	Db 179 GHEDDMPLRISYAGGIPPLEKL---LPQPRIDALVERTKGGGEVLLGGNGSAYA 233			
	246 PGASATQNAEYSLKDGRVMSVCSYLQGQYGVNHYLGVPCVIGGRGEVKIBLELAQ 305			
	Db 234 PARSLAEMVEALKDKRVLPTIALEYGBYGEVILQGCVPTIVGGNGIEQITBLETDY 292			
	305 ERQELQGSLIDEVKEMOKAI 324			
	Db 293 ERAQLNKSTVESVRNVMKAI 312			
	RESULT 8			
	S61213 malate dehydrogenase (EC 1.1.1.37) - <i>Bacillus israelii</i>			
	C;Species: <i>Bacillus israelii</i>			
	C;Date: 18-Sep-1997 #text_change 18-Sep-1997			
	C;Sequence_revision 18-Sep-1997			
	C;Accession: S61213			
	R;Myne, S.A.; Nicholls, D.J.; Scawen, M.D.; Sundaram, T.K.			
	Submitted to the EMBL Data Library, August 1995			
	A;Description: Cloning, sequence and over-expression of a tetrameric malate dehydrogenase			
	A;Reference number: S61213			
	A;Molecule type: DNA			
	A;Residues: 1-312 <WYN>			
	A;Cross-references: UNIPROT:Q59202; UNIPARC:UPI000012EE32; EMBL:X90527; NID:9963018; PID: 1048			
	A;Function: catalyzes the reversible oxidation of (S)-malate to oxalacetate by NAD			
	C;Superfamily: L-lactate dehydrogenase			
	C;Keywords: oxidoreductase			
	Query Match 43.2%; Score 729; DB 2; Length 312;			
	Best Local Similarity 44.5%; Pred. No. 1.6e-48;			
	Mismatches 69; Indels 12; Gaps 3;			
	Db 294 KATFAKSIESVRNVMKAI 311			
	RESULT 10			
	S5735 probable malate dehydrogenase (EC 1.1.1.37) - <i>Synechocystis</i> sp. (strain sll0891			
	C;Species: 2-ketoacid dehydrogenase; protein sll0891			
	C;Accession: PCC 6803			
	R;Kaneko, T.; Sato, S.; Kotani, H.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Yamada, M.; Yasuda, O.K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Yamada, M.; Yasuda, O.K.			
	DNA Res. 3, 109-136, 1996			
	A;Title: Sequence analysis of the unicellular cyanobacterium <i>Synechocystis</i> s.			
	A;Reference number: S74322; MUID:97061201; PMID:8905231			
	A;Accession: S75735			
	A;Status: nucleic acid sequence not shown; translation not shown			
	A;Molecule type: DNA			
	A;Residues: 1-324 <WAN>			
	Query 9 RPKIAMVSGMIGGTMAFLCSLRELGVVLFDV--VNMPMGKAMDISHNSVVDTG 66			
	Db 5 RKCKSVIGGFTGATAFLAKKEKLAKVVLDFIPQENPTKGAKDLMLEASPVQGEDA 64			
	67 YGSNSYECLKGADVVITAGITKIPGKSDKEWSRMDDLPVNKIMREVGAAIKSYCPNA 126			
	Db 65 IGTSNEYETADS DIVVITAGIARKPG---MSRDDLVTAGIMKAVTREVKGSPNA 119			
	127 FVINTNPFLDNVVAALQESSGLPFRHICGMAGMDSRRMERRMJDKILEVSPRDVQMVIG 186			
	Db 120 IIVVLTNPVYAMTTVYKEGFKPIRGVCGSVDLTARFRITVAQEELNVSKDTGFVLG 179			
	187 HGDDHMVPLRSRATVNGIPLSEFKVGMWIKQSEEVDDIVQTKVAGGEVRLLGQSAYA 246			
	Db 180 HGDDHMVPLRVSYAGGIPPLEKL---ERLAEIVTRKGGETVNLGGNGSAYA 234			
	247 GASIQMAMSAESYLKDGRVMSVCSYLQGQVNHLYGVPCVIGGRGEVKIBLELAQ 306			
	Db 235 AASLVEMVEAIVKDQRVLPDIALEYGEGFGLGVPTILGGNGLEQIIEELTDDEK 294			

A;Cross-references: UNIPROT:Q55383; UNIPARC:UPI000000D3536; EMBL:D64003; GB:AB001339; NID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Genetics: C;Superfamily: L-lactate dehydrogenase C;Keywords: oxidoreductase

Query Match 37.6%; Score 634; DB 2; Length 324;
Best Local Similarity 41.7%; Pred. No. 3.4e-41;
Matches 128; Conservative 66; Mismatches 103; Indels 10; Gaps 2;

Db 11 KIAMYGSGMIGGTMWFLCSLRELGVVLTEDVVPNMPGMKAMDISHNSSSVDTGTIVYGSN 70
15 QVTVVGAGVNGRTLAQLRQQNVANVVLUDIVPGPQGQALDMAAQSTYEVDSSKILGN 74

Db 16 QVTVVGAGVNGRTLAQLRQQNVANVVLUDIVPGPQGQALDMAAQSTYEVDSSKILGN 74

RESULT 12
D70444

Qy 71 SYEBCURGAGDVITIAGTIPKGSKDSREWSMDDLPVNICKMREYGAATKSYCPNAFVINI 130
Db 75 EYETAGSDVVVITAGLPRRPQ---MSRDLLGKNAIVQA CAREALRYSRNAILIV 129

Qy 131 TNPLDVMVAALQEESGLPCHRIGCAGMGLDSSRPFRRMLADKLEVSPPDQMTYGHGHDH 190
Db 130 TNPLDVMVTLIAWKVYGLPSRVMAGVLDSSRMLGACPSDINTLVGGHDL 189

Qy 191 MVPLSRYATVNGIPISFEVKKGWIKQEEVDIIVQTKTKVAGGEITVLLGGSAYAAGASA 250
Db 190 MLPLPRYCIVSGVPTIEL---IIPQTIEELVERTRNGAETAAILQNTGATVYAPASSA 244

Db 251 IOMAESYDRKDRKRVNCSCYLOOGYVQHAYLGCVIGRVEKIEITELTQAEROEIQ 310
Db 245 AVVYESILNQSRILPAATYLDGAYGLKDIFLGVPCLRCRGVEDILEVQLTPEEKALH 304

Qy 311 GSIDEVK 317
Db 305 LSAEAVR 311

RESULT 11
E70453

malate dehydrogenase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Accession: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
R;Becker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov. V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; PMID:9537320
A;Accession: E70453
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-335 <AQP>
A;Cross-references: UNIPROT:O67581; UNIPARC:UPI00000566A4; GB:AE000750; NID:92983999; PTI
A;Experimental source: strain VFS
A;Gene: mdh2
C;Genetics:
C;Superfamily: L-lactate dehydrogenase

Query Match 33.7%; Score 569; DB 2; Length 334;
Best Local Similarity 37.3%; Pred. No. 3.5e-36;
Matches 121; Conservative 76; Mismatches 101; Indels 26; Gaps 7;

Db 9 RPKIAIMVCGSGMIGGTMARLCSLRELGVVLF---DVPNMPMGKAMDISHNSSSVVDTG 63
13 KPKTSVIGAKVGENAVVLTIGLGDYLFARYKGKLEP---AKAKALDKQMAVLMQID 70

Qy 64 ITV---YGSNSYECVLKGADWVVTAGTITKIPKGSKDSKEWSRMDLPPVNTKIMREVGAAIK 119
Db 71 INVKGISYDKGEPEELKSDDIVVITAGPREG---MSREBULYENKLKFKTDIAK 125

Db 120 SYCPNAFYININTPLDVMVAALQESQSLPHHRICAGMGLDSSRFRMIADKLLEVSPRDV 179
126 EYARDTSIIIVSVNPVDTIYTATKLTGFEPRRVGMAGVLDSSRFKQFVKEKIGISNADI 185

Qy 180 QGMIVGIVGQHDMVPLSRYATVNGIPISFEVKKGWIKQBEVDIVQTKTVAGBIVRLGQ 239
Db 186 RTLVLGTHGDLAMPVTSHSFIGKPKIEEV----FASABDELIEKTRKGGAQIVSLNGT 240

Qy 240 GSAYAYPARGASATIONAEESTLKDVRKVMCSYLOGQ---YGVONHYLGVPCTVGGRYVEK 295
Db 241 -SAYYAPASVVMVNEIINDRGRMVPSSVYVEGEAAKHYEIEGVCIGLPVVLJKKGVD 299

Query Match 35.9%; Score 605.5; DB 2; Length 335;
Best Local Similarity 38.9%; Pred. No. 5.4e-39;
Matches 132; Conservative 72; Mismatches 104; Indels 31; Gaps 7;

Db 12 IAMYGSGMIGGTMWFLCSLRELGVVLFQY-----VNPNMPGKAMDISHNSSSVVDTG 64
7 VAVIGAGNNGEHVSLILRNANKMFLPRKTBEKVEPVIGKALDNKQMLAAMDDA 66

Db 65 TVYG----SNSYECVLKGADWVVTAGTITKIPKGSKDSKEWSRMDLPPVNTKIMREVGAAIK 118
67 RVEGYTVTPEGEGVPEPLESSDIVVITAGPREG---MSREBULNEANIRLVIISVIAIDI 121

Qy 119 KSYCNAFYININTPLDVMVAALQESQSLPHHRICAGMGLDSSRFRMIADKLLEVSPRD 178
Db 122 KRYAPDAIVVVTNPVDTNTYAVKLNFPKNRVMGAGVLDSSRFKTFISBELMVSFKD 181

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120	Qy	189 DHMVPRLSRYATYNGIPLSEEVKGNWIKQEEDIVQTKVAGGBIVRLLGQGSAYAFAFGA 248
A;Reference number: AB1807; MUID:2159285; PMID:1179840	Db	179 QMFPVRPLSSGGVPLHEHMSK-----EEBEVSEVNAGAKITERGY-SNNIGPA 232
A;Accession: AC2346		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-284 <KUR>		
A;Cross-references: UNIPROT:Q8YP78; UNIPARC:UPI00000CEABC; GB:BA000019; PIDN:BAB76021.1;	Qy	249 SALQMAESYLKDQRKRVNVCSCLQGQYGVQNHYLGVPCVIGGRGVKEVIELELTQAERQE 308
A;Experimental source: strain PCC 7120	Db	233 GLVLTVAEIKRDSKRIVPYSLYQGYNDIVAEPAVIGRSGIERIELPLTEDRK 292
C;Genetics:		
A;Gene: air4422	Qy	309 LQGGSIDEVKEMOKAI 323
C;Superfamily: L-lactate dehydrogenase	Db	293 FDEAQAVVKLVETL 307
Query Match Score 33.6%; DB 2; Length 284;		
Best Local Similarity 42.0%; Pred. No. 4; le-36;		
Matches 124; Conservative 54; Mismatches 90; Indels 27; Gaps 5;		
RESULT 15		
Qy 36 VVLFVVPPNPMPKAMDI-----SHNSVVDTGITYGSNSYECLKGADVVVITACIT 88		H86671 L-lactate dehydrogenase (EC 1.1.1.27) [imported] - Lactococcus lactis subsp. lactis (str
Db 1 MVLLDIVEGIPQGLALDLLEARGLTEHLNQQI-----GTINNYADTSQSQIVVITAGFP 53		C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_change 09-Jul-2004		C;Accession: H86671
Qy 89 KIPGSKSDKWSRMDLPYNIKIRVEGAIAKSYCPNAFVINITNPLDMVAAVQALQESSCLP 148		PeBoletin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Db 54 RPKG-----MSRDLILRTAKIVTEAAKQAIASPSYAIIFIVTWNPLDWTNTLAWEATCCLP 108		Genome Res. 11, 731-753, 2001
Qy 149 HHRICGMAGMLDSSRFMRNIAKDLKESPPDVQGMNIVGHGDHNVPRLSRYATYNGIPLSEF 208		A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp.
Db 109 RNRIMGMAGVLDSSARFETTALELGVLSPDKAMVLSGSGDLMPSSYYATYNGIPLTF 168		A;Reference number: A86625; MUID:21235186; PMID:11337471
Qy 209 VKKGKWIQBEVDDIVQTKVAGGBIVRLLGQGSAYAQPASASIAQMASEYLNKDRKRVNVC 268		A;Accession: H86671
Db 169 -----LDATVIERLVERTRGGABIVELNQTGAAFFAPASATSLMVSTILLNSRLLEVS 223		A;Status: preliminary
Qy 269 CYLOGQYQVNHYLGVPCVIGGRGVKEVIELELTQAQEQBQLQGSIDESVKEMOKAI 323		A;Molecule type: DNA
Db 224 YLQSEYDLDKVVGVPCLRLNLGNGIESVIBELNLSDSEREALHIS---AKSVQRNI 275		A;Residues: 1-314 <STOP>
Query Match Score 28.3%; DB 2; Length 314;		A;Cross-references: UNIPROT:Q9CII4; UNIPARC:UPI000012E2D6; GB:AE005176; PID:912273247; PI
Best Local Similarity 32.8%; Pred. No. 3.1e-29;		A;Experimental source: strain IL1403
Matches 105; Conservative 79; Mismatches 126; Indels 10; Gaps 5;		C;Genetics:
RESULT 16		C;Gene: 1dhB
probable malate dehydrogenase APB0672 - Aeropyrum pernix (strain K1)		C;Keywords: oxidoreductase
Qy	6 KTRTRPKTAMVGGCMIGGTMAFLCSRLRELGDVYLFDVUPNMMPKGKANDISHNSVVDTG 64	
Db	2 KITSRKVUVVIGTGFVGTISIAYSMINGQVNELVNUIDNQDAEGEALDLDGVSMQENV 61	
C;Accession: E72655		65 TUYGSNSYECLKGADVVVITAGITKIPGKSDEKWSRMDLPPVNMKTRVEGAIKSYCPN 124
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah		62 IVBAGDVKDC-KNADIVVVTGYNQKQG----SRDLVNTNAKMRNSIVTQVMDSGFD 115
awa, H.; Takeuchi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K		125 AFVINTNPNLDVWVAALQESSGLPHRICGMAGMLDSSRFERMIADKLEVSPRDYQGMVI 184
DNA Res. 6, 93-101, 1999		Db 116 GIFVIAASNPDVILTYAWETSGLDSKRVGTTTLDITFRKELATKLEIDPRSVHG 175
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr		
A;Reference number: A72450; MUID:99310339; PMID:10382966	Qy	185 GVKGDHMVPLSRYATVNGIPLSEF-JVKGWIQEEEDIVQTKVAGGEIVRLLGQGSAY 243
A;Accession: E72655	Db	176 GBRGDSSEAVWSHTTVCGKPILEFIVKNNKKLGVEDLSNLNKVNAAYEIID-KRQATY 233
A;Status: preliminary		
A;Molecule type: DNA		Qy 244 YAEGASAIQMQMASYLKDORKRVMVCSCLQGQYGVQHLYLGVPCVIGGRVEKLIELBTA 303
A;Residues: 1-213 <KAW>	Db	234 YGIGMSTARIVKAILNNQANIPVSAYLRGETYQGEVFTGVFSIVNQNGVREIENIDA 293
A;Cross-references: UNIPROT:Q9YEAI; UNIPARC:UPI000005DC3A; DDBJ:AP000060; NID:95104188;		
A;Experimental source: strain K1	Qy	304 QERQELQSIDEVKEMOKAI 323
C;Genetics:	Db	294 YERKQFERSVSQLEKIESI 313
A;Gene: APE0672		Search completed: March 2, 2006, 19:40:42
C;Superfamily: L-lactate dehydrogenase		Job time : 25 secs
Query Match Score 33.2%; DB 2; Length 313;		
Best Local Similarity 35.9%; Pred. No. 1.4e-35;		
Matches 113; Conservative 72; Mismatches 119; Indels 11; Gaps 3;		
RESULT 17		
Qy 9 RPKIAMVGGCMIGGTMAFLCSRLRELGDVYLFDVUPNMMPKGKANDISHNSVVDTG 68		
Db 4 QPLITLGAKGVNATAVNMURMRSYDLDLILIAARTPGKPGPEADELDLAHAELGVDIR 63		
C;Accession: E72655		
Qy 69 SNSYECLKGADVVVITAGITKIPGKSDEKWSRMDLPPVNMKTRVEGAIKSYCPN 128		
Db 64 SNSYEDMRSSEDIVVYTAGTGRKPG-----MTREQLLEANANTMADLKTIKAYAKDADV 118		
A;Cross-references: UNIPROT:Q8SSGP; HHRICGMAGMLDSSRFERMIADKLEVSPRDYQGMVI 188		
A;Experimental source: strain K1	Qy	129 NITNPLDVVAALQESSGLPHRICGMAGMLDSSRFERMIADKLEVSPRDYQGMVI 178
C;Genetics:	Db	119 ITINPVDAINTVMMYKKTPGPRERVIGFSGILDSSARMAYVISQKLGVSPKSNRAVLMGH 178

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:37:51 ; search time 185 Seconds

(without alignments)
 783.757 Million cell updates/sec

Title: US-09-390-846-2
 Perfect score: 1688

Sequence: 1 MAVFERKTRPKIAMVSGM1.....GSIDEVKEMOKAIALDASK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
 Maximum Match 100\$
 Listing first 45 summaries

Database : A_Geneseq_21:
 1: _geneseqp1980s:
 2: _geneseqp1990s:
 3: _geneseqp2000s:
 4: _geneseqp2010s:
 5: _geneseqp2002s:
 6: _geneseqp2003as:
 7: _geneseqp2003bs:
 8: _geneseqp2004s:
 9: _geneseqp2005s:
 AAW11476 standard; protein; 330 AA.

RESULT 1

AAW11476

ID XX

AC XX

DT 17-OCT-2003

(revised)

DT 29-APR-1997

(first entry)

XX Eimeria lactate dehydrogenase.

DE XX

KW Lactate dehydrogenase; LDH; coccidiosis; vaccine; vector.

XX OS Eimeria acervulina; strain Houghton.

XX PN AU956287-A.

XX PD 16-JAN-1997.

XX PF 02-JUL-1996;

XX PR 03-JUL-1995;

XX PA (ALKO) AKZO NOBEL NV.

XX PI Kok JJ, Van Den Boogaart P, Vermeulen AN;

XX DR WPI:1997-109375/11.

XX N-PSDB; AAT51370.

XX PR 96AU-00056287.

XX PR 95EP-00201801.

XX

ALIGNMENTS

Ad522139 Bacterial

Ad530817 Bacterial

Adn20169 Bacterial

Adn2111 Bacterial

XX	US2003233675-A1.	Db	238 SATEMAESYLKDCKVLPAAHLSGGQYGDMDYVGPFITIAGGIERVIEELNKEEAA	297
XX	PD 1B-DEC-2003.	Qy	309 LQGSSIDEVKEMORA	322
XX	20-FEB-2003; 2003US-00369493.	Db	298 FQKSVGAVAGLCEA	311
XX	21-FEB-2002; 2002US-0360039P.			
XX	(CAOY/) CAO Y.	RESULT 4		
PA	(HINK/) HINKLE G. J.	ID ADS25456 Standard; protein;	320 AA.	
PA	(SLAT/) SLATER S. C.	XX		
PA	(CHEN/) CHEN X.	AC		
PA	(GOLD/) GOLDMAN B. S.	ADS25456;		
XX	PI Cao Y., Hinkle GJ, Slater SC, Chen X., Goldman BS;	XX		
XX	DR WPI; 2004-061375/06.	DT 02-DEC-2004 (first entry)		
XX	PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.	DE Bacterial polypeptide #14489.		
XX	PS SEQ ID NO 11441; 122pp; English.	XX		
CC	CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.	XX		
CC	CC Sequence 319 AA;	XX		
CC	CC Query Match 51.7%; Score 873.5; DB 8; Length 319;	XX		
CC	CC Best Local Similarity 53.2%; Pred. No. 8.1e-78;	XX		
CC	CC Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;	XX		
Qy	9 RPKIAMVGGMIGGTMAFFLSSLRELGDVLFDVVPNNPMKGANDISHNSVVDTGTVYG	68		
Db	3 RKKIALIGSMIGGTLLAHASLKELGDIVLFDAIDGIPQKGKLDIQSPGPVEGNALSG	62		
Qy	69 SNSYECILKADVVITAGITKIPGSKSDKWSRMDLPVNIKIMREVGAIAKSYCPNAFV	128		
Db	63 ASDVAIIEGADCVLTAGARKPS----MSRDPLLGINLKVMBQVGAKIKYAPNAFV	117		
Qy	129 NITNPFLDVMVAAQLEQSSGLPHHRICGMAGMIDSSRFERMIAKLEVSPRDVGFMVIGYH	188		
Db	118 CITNPFLDAMVWALQKFSGIPLPNKIVGMAVLDSARFLFLAEFFNVSYQDVTAFVLGCHG	177		
Qy	189 DHMVPFLSRVATVNGIPLSPEFVKRKGWIKQFBDLVQKTKVAGGBIVRLQGQSAYAYFGA	248		
Db	178 DTMVPLARSTVGGVPLTLVQMGWLTAERLEQIQTTRDGAEITVGLKTGSAYAYAPA	237		
Qy	249 SAQMAESTLKDRKRVMYCSCLQYQGYQNHYLGVPVIGGRGEVKIIELELTQAERQE	308		

CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX New recombinant DNA construct comprising a promoter positioned to provide
 XX expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
 XX

SQ Sequence 320 AA;

Query Match	51.7%	Score	873.5	DB	8	Length	320;			
Best Local Similarity	53.2%	Pred.	No.	8.1e-78;	Mismatches	60;	Indels	5;	Gaps	1;
Matches	167;	Conservative	60;							

Qy 9 RPKIAMVGGSGMIGGTTMAFICSLREIGDVYLPVNPMKGAMDISHNSWVDTGITYTG 68
 Db 3 RKKALIGSGMIGGTLAHLASLRLGDIYLDIADGIPOGKGLDIAQGPVEGENAKLSG 62

Qy 69 SNSYECLKGADVVITAGITKIPGKSDKNEWSRMDLLPVNIKINBEVGAAIKSKCPNAFVI 128
 Db 63 ASDAAIEGADVDC1VTAGARKPG----MSRDDLGIGNLKMEQVGAIIKYAPNAFVI 117

Qy 129 NITNPOLDWVVAALQESSGLPHHR1CGMAGMLDSSEFRMIAKLESPRDVQGMVIGHG 188
 Db 118 CITNPLDAWVVAALQKFSGPKPNKVGMAGVLDARFLAERFLAEFFENVSQDVTAFULSGH 177

Qy 189 DHMVLPLSRATVNGIPLSBEPKRKWIKOBEDVIVQKTPVAGGBIVRLJGOGSAYYAPGA 248
 Db 178 DTMPLARISTVGGYPLTIVLKVKGWLARBLEQIQRTRDGGEIVGLKTGSAYAYPA 237

Qy 249 SATQMAESTLKDRKRVMVCSYLOGQYQXNHVLYGVPYCIGGGVKEVTKTELETTAQERQE 308
 Db 238 SATQMAESTLKDRKRVLPAAHLSQYGVDDMTVGVPTIGAGGIERVIEBLNEKEAA 297

Qy 309 LGSSIDEVEMOKA 322

Db 298 FQKSVGAVAGLCEA 311

SQ Sequence 320 AA;

Query Match	51.7%	Score	873.5	DB	8	Length	320;			
Best Local Similarity	53.2%	Pred.	No.	8.1e-78;	Mismatches	60;	Indels	5;	Gaps	1;
Matches	167;	Conservative	60;							

Qy 9 RPRIAMYGSMIGGTTMAFICSLREIGDVYLPVNPMKGAMDISHNSWVDTGITYTG 68
 Db 3 RKKALIGSGMIGGTLAHLASLRLGDIYLDIADGIPOGKGLDIAQGPVEGENAKLSG 62

Qy 69 SNSYECLKGADVVITAGITKIPGKSDKNEWSRMDLLPVNIKINBEVGAAIKSKCPNAFVI 128
 Db 63 ASDAAIEGADVDC1VTAGARKPG----MSRDDLGIGNLKMEQVGAIIKYAPNAFVI 117

Qy 129 NITNPOLDWVVAALQESSGLPHHR1CGMAGMLDSSEFRMIAKLESPRDVQGMVIGHG 188
 Db 118 CITNPLDAWVVAALQKFSGPKPNKVGMAGVLDARFLAERFLAEFFENVSQDVTAFULSGH 177

Qy 189 DHMVLPLSRATVNGIPLSBEPKRKWIKOBEDVIVQKTPVAGGBIVRLJGOGSAYYAPGA 248
 Db 178 DTMPLARISTVGGYPLTIVLKVKGWLARBLEQIQRTRDGGEIVGLKTGSAYAYPA 237

Qy 249 SATQMAESTLKDRKRVMVCSYLOGQYQXNHVLYGVPYCIGGGVKEVTKTELETTAQERQE 308
 Db 238 SATQMAESTLKDRKRVLPAAHLSQYGVDDMTVGVPTIGAGGIERVIEBLNEKEAA 297

Qy 309 LGSSIDEVEMOKA 322

Db 298 FQKSVGAVAGLCEA 311

RESULT 5
 ADS25841 standard: protein; 320 AA.

XX

AC ADS25841;

XX DT 02-DEC-2004 (first entry)

XX DB Bacterial polypeptide #14874.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 OS Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039D.
 XX PD (CAO Y., CAO Y.,
 XX PA (HINKLE G. J., HINKLE G. J.,
 XX PA (SLATER S. C., SLATER S. C.,
 XX PA (CHEN X., CHEN X.,
 XX PA (GOLDMAN B. S., GOLDMAN B. S.,
 XX PR (ADS42318 standard; protein; 311 AA.
 XX ID ADS42318
 XX AC ADS42318;
 XX DT 02-DEC-2004 (first entry)
 XX DE Bacterial polypeptide #20748.
 XX KW Recombinant DNA construct; transformed plant; improved plant property;

XX 309 LGSSIDEVEMOKA 322
 DB 298 FQKSVGAVAGLCEA 311

RESULT 6
 ADS42318
 ID ADS42318
 XX AC ADS42318;
 XX DT 02-DEC-2004 (first entry)
 XX DE Bacterial polypeptide #20748.
 XX KW Recombinant DNA construct; transformed plant; improved plant property;

cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX

Bacteria.

US200323675-A1.

XX

PD 18-DEC-2003.

XX

PF 20-FEB-2003; 2003US-00369493.

XX

PR 21-FEB-2002; 2002US-03600398.

XX

WPI; 2004-061375/06.

XX

PT New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX

Claim 1; SEQ ID NO 20748; 122pp; English.

XX

The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil and/or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the

CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic

CC format from USPROT seqdate.uspto.gov/sequence.html.

XX

SQ Sequence 311 AA;

PS

XX

Query Match

Best Local Similarity

Matches 169; Conserved

Score 862.5; DB 8;

Length 311;

Pred. No. 9_7e-77;

Mismatches 59;

Indels 5;

Gaps 1;

XX

CC

CC increased resistance to plant disease; better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators; increased rate of
 CC homologous recombination; modified seed oil or protein yield and/or
 CC content; improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake; by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition; improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 322 AA;

Query Match 51.1%; Score 862; DB 8; Length 322;
 Best Local Similarity 53.5%; Pred. No. 1.e-76;
 Matches 174; Conservative 56; Mismatches 87; Indels 8; Gaps 2;
 Qy 9 RPKIAMVGGMIGTMAPLCSRELGDVLFDPVNPNPMGKAMDISNSVVDTGTVYG 68
 Db 3 RNKALIGSMIGGTLLAHMIGKLDGVLFDAIGPQKGKDASSPVDFGSRLTG 62
 Qy 69 SNSYECLKGADVVITTAGTICPKGSDEKWSRMDLPPVNKIMREVGAAIKSYCPNAFVI 128
 Qy 63 VNDYAGIGADCVITAGVPRKG---MSRDDLGINLKWMEQVAGLKXKAPKA FVI 117
 Qy 129 NITNPFLDVMVAALQESSCPHHRICGMAGMLJSSSRFERMIAKLEVSPRDVQGMUTGVHG 188
 Db 118 .CITNPLDAMWALQKFSSGIPKTHVVGMAVLDSARFYFLABEFKVSVEDTAFVLCGHG 177
 Qy 169 DHMVPRLSRAYATNGIPISEPVKKGWIKEBVDDIVQTKTKVAGEIVBLQGOSAYAAPA 248
 Qy 178 DSKVPMTRYSITVSGIPLDVLVKMGWTSEKLQIVQRTDGAAIVVCLLKTSAYAAPA 237
 Db 249 SAQMAESYLQDKRVMVSCYTLQGOYGVQHNLGVCPVIGGRGEVKIIELTLTAQEROE 308
 Qy 238 SAQMAESYLQDKRVLPCAAHLSGQITGVKGTIVGVPIVAGGVERIEIDLNKSEQKM 297
 Qy 309 LOGSIDEYKEMOKA--'IAJADASK 330
 Db 298 FESSVATVQGLTBACVKIAPOLASK 322

RESULT 8

ADS28046 standard; protein; 320 AA.

XX ADS28046;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #17079.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS US200333675-A1.
 PN XX 18-DEC-2003.
 PD XX 20-FEB-2003; 2003US-00369493.
 PR XX 21-FEB-2002; 2002US-0360039P.
 PA XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX DR WPI; 2004-061375/06.
 XX PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX PS SEQ ID NO 17079; 1229bp; English.
 XX

CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polypeptide from a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/Sequence.html.
 XX SQ Sequence 320 AA;

Query Match 50.4%; Score 850 5; DB 8; Length 320;
 Best Local Similarity 51.1%; Pred. No. 1.6e-75;
 Matches 164; Conservative 60; Mismatches 92; Indel 8 5; Caps 1;
 Qy 9 RPKIAMVGGMIGTMAPLCSRELGDVLFDPVNPNPMGKAMDISNSVVDTGTVYG 68
 Db 3 RAKIALIGSMIGGTLLAHMIGKLDGVLFDAIGPQKGKDASSPVDFGSRLTG 62
 Qy 69 SNSYECLKGADVVITTAGTICPKGSDEKWSRMDLPPVNKIMREVGAAIKSYCPNAFVI 128
 Db 118 .ANDYADIAQADCVITAGVPRKG---MSRDDLGINLKWMEQVAGLKXKAPKA FVI 117
 Qy 169 NTINPLDVMVAALQESSCPHHRICGMAGMLJSSSRFERMIAKLEVSPRDVQGMUTGVHG 188
 Db 178 DDMPVPHSTVGGLPLPELYVKQNLSDQKLDIAVERTTRKGGEITVALLXKTGSASFVAPAE 237
 Qy 249 SAQMAESYLQDKRVMVSCYTLQGOYGVQHNLGVCPVIGGRGEVKIIELTLTAQEROE 308
 Db 238 CITNPLDAMWALQKFSSGIPKTHVVGMAVLDSARFYFLABEFKVSVEDTAFVLCGHG 177
 Qy 298 SAIQMAESYLQDKRVMVSCYTLQGOYGVQHNLGVCPVIGGRGEVKIIELTLTAQEROE 308
 Db 238 SAIAMATSYLDKRVLPCTVLTGQYGLNDLYVGTVVAGGAAKIVEFETNDDEKAM 297

RESULT 9
 ID ADN25360
 ID ADN25360 standard; protein; 320 AA.
 ID ADN25360;

PR 309 LGQSIDEVKEMOKATAALDAS 329
 PR 298 FAKSVESVKGIMEACKAIDSS 318

RESULTS 9
 ID ADN25360
 ID ADN25360 standard; protein; 320 AA.

XX ADN25360; AC ADN25360; DB 02-DEC-2004 (first entry) XX Bacterial polypeptide #8013.

KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; Plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

XX Bacteria. XX US2003233675-A1. XX 18-DEC-2003. XX 20-FEB-2003; 2003US-00369493. XX 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y. PA (HINK/) HINKLE G J. PA (SLAT/) SLATER S C. PA (CHEN/) CHEN X. PA (GOLD/) GOLDMAN B S.

PI Cao Y., Hinkle GJ., Slater SC., Chen X., Goldman BS.; XX DR; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 8013; 122PP; English.

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway or improved plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 320 AA;

Query Match 50.3%; Score 848.5; DB 8; Length 320; Best Local Similarity 50.8%; Pred. No. 2.5e-75; Matches 163; Conservative 64; Mismatches 89; Indels 5; Gaps 1;

SQ 9 RPKIAMVGSGMIGSTMAFFCSLRLBDGVVLPNNMKGKMDISHNSVVDTGITYVG 68

Db 3 RPKIALIGAQIQGQTALAAIKELGDVVLFDIAEGTPOGKALDIAQSGPSEGFDAMKG 62

Qy 69 SNEYECBLKGADYVITAGTICKINGSKDSKEWSRDLPLPNIKINREVGAIKSCKPNAPFTI 128

Db 63 ANSYEBIGADCVTAVGPKEKG----MSRDLLGILNKWPKSVGBGIKAHPNAFTI 117

Db 129 NITNPDLDMVAALQESSGLPHHRICGMGLDSSRFRFMRMIADKLEVSPRDVQGMIVGYHG 188

Qy 118 CITNPDLDMVAALQESSGLPHHRICGMGLDSSRFRFMRMIADKLEVSPRDVQGMIVGYHG 177

Db 189 DAVNPLSRYATNGIPLSBFVKKGWIKOEVDDIVQTKVAGGEIVRLLGQSAYAYGA 248

Qy 178 DTAVPLVRYSTVAGIPLPDLVQNGWTQEKLDIVQPRDGAEIVGLKTGSAYFAPAT 237

Qy 249 SATQMAESEYLKDOKRVMCKSCYLVQGOTGVQVNEHYLGYPECIVGRGVKEIELETAAQEQQ 308

Db 238 SATEMAEAYLKDKORLPCAYTDGFLGLNGMTVGVPTIAGGIEKIVDIKUNDDEQAM 297

Qy 309 LQGSIDEVKEMKQAKAALDAS 329

Db 298 FDKSVANAVTKGLVEACKGIDSS 318

RESULT 10 ADS21490 ID ADS21490 standard; protein; 320 AA.

XX XX XX AC ADS21490;

XX XX DT 02-DEC-2004 (first entry)

XX XX DE Bacterial polypeptide #10523.

XX XX Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

XX XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX XX CAO Y. PA (HINK/) HINKLE G J. PA (SLAT/) SLATER S C. PA (CHEN/) CHEN X. PA (GOLD/) GOLDMAN B S.

XX PI Cao Y., Hinkle GJ., Slater SC., Chen X., Goldman BS.; XX DR; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX XX CAO Y. PA (HINK/) HINKLE G J. PA (SLAT/) SLATER S C. PA (CHEN/) CHEN X. PA (GOLD/) GOLDMAN B S.

XX PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX XX CAO Y. Hinkle GJ., Slater SC., Chen X., Goldman BS.; XX DR; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX XX CAI 1; SEQ ID NO 10523; 122PP; English.

XX XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway or improved plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 320 AA;

CC Query Match 50.3%; Score 848.5; DB 8; Length 320; Best Local Similarity 50.8%; Pred. No. 2.5e-75; Matches 163; Conservative 64; Mismatches 89; Indels 5; Gaps 1;

CC 9 RPKIAMVGSGMIGSTMAFFCSLRLBDGVVLPNNMKGKMDISHNSVVDTGITYVG 68

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a

transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence	320 AA;	Query Match	50.2% ; Score 847.5 ; DB 8 ; Length 320 ;	Best Local Similarity	52.0% ; Pred. No. 3.1e-5 ;	Mismatches	61 ; Indels	Gaps	1
Y	Matches 167 ; Conservative	9 RPKIANYGSGMIGGMATMAFLCSLRELGDVVLFDVPPNPMGKADMIDCHNSSVYDGTITVY 68	b	3 RKKAGLAGNIGGTTAHLAAQKELDIDVLPVBBGPQKGALDSQCGPVGFIDANIG 62					
Y		69 SNSYCLKGADWVITAGITKIPGKSDKEWSRMDDLPVNKIMRENGAAIKSYCPNAFVI 128	b						
Y		63 TNDYKIAAGDVIITAGVARKPG----MSRDDLGGINLKUMKAVEGEGRDNAPDAFVI 117	b						
Y		129 NITNPUDVMVAALQESGLPHRICAGMGLDSRRPMTIADKLBEVSPRDYQGMVYGVHVG 188	b						
Y		118 CITNPUDAMTWALEFGSLPANKVGMAGVLDSSARSTFLAMEFGVSIRDNTFVLGGHG 177	b						
Y		189 DHMVPILSRYATVNGPLSEFYTKGNKQEEYVIVDIOVTKVYAGGETRLLGCGSATAYPGA 248	b						
Y		178 DTMVPQTQSYTVNGLPVDLVKRMGSQEKAIDAVTRRSGGTEVGLKTGSFAFAPAA 237	b						
Y		249 SAIQMAESYLSVKDRKVMWVCSCLYLOGQGYVQNHLYGYPVCIVGGRGVKEKIELELTQAERQE 308	b						
Y		238 SGIANAEAYINDQRILPCAYVGDGYGVNGLYVGVPLIGANGVEKVIETEFLDEAKGN 297	b						
Y		309 LOGSDEVKEMQKAALDAS 329	b						
Y		298 LOVSDDAVKELIETAKGIDPS 318	b						

PR 12-APR-1993; 93US-00046160.
 XX (DART-) DARTMOUTH COLLEGE.
 PA XX
 PI Bzik DJ, Fox BA;
 XX DR WPI: 1994-341866/42.
 XX DR N-PSDB; AA072947.
 PT Isolated gene encoding lactate
 XX PT methods for diagnosis and vac-
 PS Claim 5; Page 18-19; 35pp; En-
 XX This sequence represents P. f.
 CC LDH protein and immunogenic f.
 CC for antibody generation. The
 CC detection of antibody titres
 CC against fragments of LDH can
 CC be used to detect the presence
 CC of antibodies to the isolated
 CC gene product.

Db	302	FDEAIAETKRMK	313
		RESULT 12	
		AAY01690	
	ID	AAY01690 standard; protein; 3	
	XX		
	AC	AAY01690;	
	XX		
	DT	23-JUN-1999 (first entry)	
	XX		
	DE	A Plasmodium falciparum lactate dehydrogenase; LDH; a	
	XX		
	KW	Lactate dehydrogenase; LDH; a immunization; Plasmodium falciparum.	
	KW		
	OS	Plasmodium falciparum.	
	XX		
	PN	W09913903-A1.	
	XX		
	PD	25-MAR-1999.	
	XX		
	PF	08-SEP-1998;	
	XX		
		98WO-US0188626.	

This sequence represents a protein having heat resistant maleate dehydrogenase (h-RMAD) activity. The protein has a residual activity after storage at 40 deg.C for 10 days of at least 60%, pref. 70% and esp. 90%. A reagent containing the h-RMAD protein, NADH and L-aspartic and alpha-ketoglutaric acid may be used for the determination of glutamine oxalo-transaminase (GOT) activity. The h-RMAD protein may be produced by transforming E. coli with the DNA encoding this protein and isolating the protein from the culture medium. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 329 AA;

Query	Match	Score	705;	DB	2;	Length	329;		
Best	Local Similarity		41.8%;	Pred.	No.	3.9e-61;			
Matches	136;	Conservative	45.3%;	Mismatches	88;	Indels	12;	Gaps	3;
Db									
Qy	9 RPKIAMVGSIGMIGGTMAFLCSSLRLRELGVYVLFDV--VPNNPMGKAMDISHNSNNSVYDTGITY	66							
	5 RKKLISVIGAGFTGAAFTAFLAQKELGDWVLVDIPOLENNTKGRAIDMLASPVLGFDANI	64							
Qy	67 YGSNSYECIKGADYVLTAGITKIPGKSDEKEWSRMDILPWNKIMREVGAIKSYCPNRF	126							
Db	65 IGTSDYADTADS DIVVITGIAKREG----MSRDLVTTNOKIMKOVTKEVVKYSPNRY	119							
Qy	127 VINTNPNDWVAALQESSSLPHHRICGAAGMLDSSRFRMIAKDLLEVPRDYGGMVIGV	186							
Db	120 IIVLTNPVDAMTYTFKESFPQNREVIGQSGVLDTARFRTFVARELNITSKVDTGFVLG	179							
Qy	187 HGDDHMVPLSRSRATYNGIPIPLSEBFVKKGWIROBEYDIVKTKVAGGEIVRLGGSSAYYAP	246							
Db	180 HGDDHMVPLRYSAGGIPLKLIPK---DRLDIAVETRKGGGEIVNLGNGSAYYAP	234							
Qy	247 GASALQMAEASYLKDKRKVNVCSCVLLQQYQVQNEHYLGPCVIGGRGEVKIEBLTAQF	306							
Db	235 AASLIVEMVAILKQRRILPAIAVLEGEIYGEGIYLGVPTILGNGNGIEVKIELELTESEK	294							

Search completed: March 2, 2006, 19:44:28
 Job time : 188 secs

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